

GTTTAGTCTGCAGCCGAGCAGCTAAAGGAGAAAGAATCGCTCAGGAAAGACACACTGCAGACTCCACGGCACCCCTGC	79
AATAGATGGGTTCCGACTACACAAAGGAGAAAACGCGAGGTGACACTCTCCTGCTGGAAGAGGACGAAACGACCAAA	158
CAAACGCAAGGACTGGACTCCATGCCGAAGGTATCTGGAAGTCGTGACACCGTGTGTATATAACAAAAGTTTGCGAGCT	237
GTTAATTGCTGTGCTGTATTATTAAGAGACGCTTTCAAGTTTCAAGTACCAAAATGTAGCTTTACGTTGCCAAAGGAAAGT	316
TGAGGCAATTGCTTTGCTGTTTAACTTGCTCTGTGAGGAAATCTCATAAACTGACCA ATG CAC CAA ATG AAT	5- 390
A K M H F R F V F A L L I V S F N H D V	25
GCT AAA ATG CAC TTT AGG TTT GTT TTT GCA CTT CTG ATA GTA TCT TTC AAC CAC GAT GTA	450
L G K N L K Y R I Y E E Q R V G S V I A	45
CTG GGC AAG AAT TTG AAA TAC AGG ATT TAT GAG GAA CAG AGG GTT GGA TCA GTA ATT GCA	510
R L S E D V A D V L L L K L P N P S T V R	65
AGA CTA TCA GAG GAT GTG GCT GAT GTT TTA TTG AAG CTT CCT AAT CCT TCT ACT GTT CGA	570
F R A M Q R G N S P L L L V V N E D N G E	85
TTT CGA GCC ATG CAG AGG GGA AAT TCT CCT CTA CTT GTA GTA AAC GAG GAT AAT GGG GAA	630

Fig. 1A

I	S	I	G	A	T	I	D	R	E	Q	L	C	Q	K	N	L	N	C	S	105	
ATC	AGC	ATA	GGG	GCT	ACA	ATT	GAC	CGT	GAA	CAA	CTG	TGC	TGC	CAG	AAA	AAC	TTG	AAC	TGT	TCC	690
I	E	F	D	V	I	T	L	P	T	E	H	L	Q	L	F	H	I	E	V	125	
ATA	GAG	TTT	GAT	GTG	ATC	ACT	CTA	CCC	ACA	GAG	CAT	CTG	CAG	CTT	TTC	CAT	ATT	GAA	GTT	750	
E	V	L	D	I	N	D	N	S	P	Q	F	S	R	S	L	I	P	I	E	145	
GAA	GTG	CTG	GAT	ATT	AAT	GAC	AAT	TCT	CCC	CAG	TTT	TCA	AGA	TCT	CTC	ATA	CCT	ATT	GAG	810	
I	S	E	S	A	A	V	G	T	R	I	P	L	D	S	A	F	D	P	D	165	
ATA	TCT	GAG	AGT	GCA	GCA	GTT	GGG	ACT	CGC	ATT	CCC	CTG	GAC	AGT	GCA	TTT	GAT	CCA	GAT	870	
V	G	E	N	S	L	H	T	Y	S	L	S	A	N	D	F	F	N	I	E	185	
GTT	GGG	GAA	AAT	TCC	CTC	CAC	ACA	TAC	TCG	CTC	TCT	GCC	AAT	GAT	TTT	TTT	AAT	ATC	GAG	930	
V	R	T	R	T	D	G	A	K	Y	A	E	L	I	V	V	R	E	L	D	205	
GTT	CGG	ACC	AGG	ACT	GAT	GGA	GCC	AAG	TAT	GCA	GAA	CTC	ATA	GTG	GTC	AGA	GAG	TTA	GAT	990	
R	E	L	K	S	S	Y	E	L	Q	L	T	A	S	D	M	G	V	P	Q	225	
CGG	GAG	CTG	AAG	TCA	AGC	TAC	GAG	CTT	CAG	CTC	ACT	GCC	TCA	GAC	ATG	GGA	GTA	CCT	CAG	1050	
R	S	G	S	S	I	L	K	I	S	I	S	D	S	N	D	N	S	P	A	245	
AGG	TCT	GGC	TCA	TCC	ATA	CTA	AAA	ATA	AGC	ATT	TCA	GAC	TCC	AAT	GAC	AAC	AGC	CCT	GCT	1110	

Fig. 1B

F	E	Q	Q	S	Y	I	I	I	Q	L	L	E	N	S	P	V	G	T	L	L	265
TTT	GAG	CAG	CAA	TCT	TAT	ATA	ATA	CAA	CTC	TTA	GAA	AAC	TCC	CCG	GTT	GGC	ACT	TTG	CTC	1170	
L	D	L	N	A	T	D	P	D	E	G	A	N	G	K	I	V	Y	S	F	285	
TTA	GAT	CTG	AAT	GCC	ACG	GAT	CCA	GAT	GAG	GGC	GCT	AAT	GGG	AAA	ATT	GTA	TAT	TCC	TTC	1230	
S	S	H	V	S	P	K	I	M	E	T	F	K	I	D	S	E	R	G	H	305	
AGC	AGT	CAT	GTG	TCT	CCC	AAA	ATT	ATG	GAG	ACT	TTT	AAA	ATT	GAT	TCT	GAA	AGA	GGA	CAT	1290	
L	T	L	F	K	Q	V	D	Y	E	I	T	K	S	Y	E	I	D	V	Q	325	
TTG	ACT	CTT	TTC	AAG	CAA	GTG	GAT	TAT	GAA	ATC	ACC	AAA	TCC	TAT	GAG	ATT	GAT	GTT	CAG	1350	
A	Q	D	L	G	P	N	S	I	P	A	H	C	K	I	I	I	K	V	V	345	
GCT	CAA	GAT	TTG	GGT	CCA	AAT	TCA	ATC	CCA	GCC	CAT	TGC	AAA	ATT	ATA	ATT	AAG	GTT	GTG	1410	
D	V	N	D	N	K	P	E	I	N	I	N	L	M	S	P	G	K	E	E	365	
GAT	GTT	AAT	GAC	AAT	AAA	CCT	GAA	ATT	AAC	ATC	AAC	CTC	ATG	TCC	CCT	GGA	AAA	GAA	GAA	1470	
I	S	Y	I	F	E	G	D	P	I	D	T	F	V	A	L	V	R	V	Q	385	
ATA	TCT	TAT	ATT	TTT	GAA	GGG	GAT	CCT	ATT	GAT	ACA	TTT	GTT	GCT	TTG	GTC	AGA	GTT	CAG	1530	
D	K	D	S	G	L	N	G	E	I	V	C	K	L	H	G	H	G	H	F	405	
GAC	AAG	GAT	TCT	GGG	CTG	AAT	GGA	GAA	ATA	GTT	TGT	AAG	CTT	CAT	GGA	CAT	GGT	CAC	TTT	1590	

Fig. 1C

K	L	Q	K	T	Y	E	N	N	Y	L	I	L	T	N	A	T	L	D	R	425
AAA	CTT	CAG	AAG	ACA	TAT	GAA	AAC	AAT	TAT	TTA	ATC	TTA	ACT	AAT	GCC	ACA	CTG	GAT	AGA	1650
E	K	R	S	E	Y	S	L	T	V	I	A	E	D	R	G	T	P	S	L	445
GAA	AAG	AGA	TCT	GAG	TAT	AGT	TTG	ACT	GTA	ATC	GCT	GAG	GAC	AGG	GGG	ACA	CCC	AGT	CTC	1710
S	T	V	K	H	F	T	V	Q	I	N	D	I	N	D	N	P	P	H	F	465
TCT	ACA	GTG	AAA	CAT	TTT	ACA	GTT	CAA	ATC	AAT	GAT	ATC	AAT	GAC	AAT	CCA	CCC	CAC	TTC	1770
Q	R	S	R	Y	E	F	V	I	S	E	N	N	S	P	G	A	Y	I	T	485
CAG	AGA	AGC	CGA	TAT	GAA	TTT	GTA	ATT	TCA	GAA	AAT	AAC	TCA	CCA	GGG	GCA	TAT	ATC	ACC	1830
T	V	T	A	T	D	P	D	L	G	E	N	G	Q	V	T	Y	T	I	L	505
ACT	GTT	ACA	GCC	ACA	GAT	CCT	GAT	CTT	GGA	GAA	AAT	GGG	CAA	GTG	ACA	TAC	ACC	ATC	TTG	1890
E	S	F	I	L	G	S	S	I	T	Y	T	V	T	I	D	P	S	N	G	525
GAG	AGT	TTT	ATT	CTA	GGA	AGT	TCC	ATA	ACT	ACA	TAT	GTA	ACC	ATT	GAC	CCA	TCT	AAT	GGA	1950
A	I	Y	A	L	R	I	F	D	H	E	E	V	S	Q	I	T	F	V	V	545
GCC	ATC	TAT	GCC	CTC	AGA	ATC	TTT	GAT	CAT	GAA	GAA	GTG	AGT	CAG	ATC	ACT	TTT	GTG	GTA	2010
E	A	R	D	G	G	S	P	K	Q	L	V	S	N	T	T	V	V	L	T	565
GAA	GCA	AGA	GAT	GGA	GGA	AGC	CCG	AAG	CAA	CTG	GTA	AGC	AAT	ACC	ACA	GTT	GTG	CTC	ACC	2070

Fig. 1D

I	I	D	E	N	D	N	V	P	V	V	I	G	P	A	L	R	N	N	T	585
ATC	ATT	GAC	GAA	AAT	GAC	AAC	GTT	CCT	GTG	GTT	ATA	GGG	CCT	GCA	TTG	CGT	AAT	AAT	ACG	2130
A	E	I	T	I	P	K	G	A	E	S	G	F	H	V	T	R	I	R	A	605
GCA	GAA	ATC	ACC	ATT	CCC	AAA	GGG	GCT	GAA	AGT	GGC	TTT	CAT	GTC	ACA	AGA	ATA	AGG	GCA	2190
I	D	R	D	S	G	V	N	A	E	L	S	C	A	I	V	A	G	N	E	625
ATT	GAC	AGA	GAC	TCT	GGT	GTG	AAT	GCT	GAA	CTC	AGC	TGC	GCC	ATA	GTA	GCA	GGT	AAT	GAG	2250
E	N	I	F	I	I	D	P	R	S	C	D	I	H	T	N	V	S	M	D	645
GAG	AAT	ATC	TTC	ATA	ATT	GAT	CCA	CGA	TCA	TGT	GAC	ATC	CAT	ACC	AAC	GTT	AGC	ATG	GAT	2310
S	V	P	Y	T	E	W	E	L	S	V	I	I	Q	D	K	G	N	P	Q	665
TCT	GTT	CCC	TAC	ACA	GAA	TGG	GAG	CTG	TCA	GTT	ATC	ATT	CAG	GAC	AAA	GGC	AAT	CCT	CAG	2370
L	H	T	K	V	L	L	K	C	M	I	F	E	Y	A	E	S	V	T	S	685
CTA	CAT	ACC	AAA	GTC	CTT	CTG	AAG	TGC	ATG	ATC	TTT	GAA	TAT	GCA	GAG	TCG	GTG	ACA	AGT	2430
T	A	M	T	S	V	S	Q	A	S	L	D	V	S	M	I	I	I	I	S	705
ACA	GCA	ATG	ACT	TCA	GTA	AGC	CAG	GCA	TCC	TTG	GAT	GTC	TCC	ATG	ATA	ATA	ATT	ATT	TCC	2490
L	G	A	I	C	A	V	L	L	V	I	M	V	L	F	A	T	R	C	N	725
TTA	GGA	GCA	ATT	TGT	GCA	GTG	TTG	CTG	GTT	ATT	ATG	GTG	CTA	TTT	GCA	ACT	AGG	TGT	AAC	2550

Fig. 1E

R	E	K	K	D	T	R	S	Y	N	C	R	V	A	E	S	T	Y	Q	H	745
CGC	GAG	AAG	AAA	GAC	ACT	AGA	TCC	TAT	AAC	TGC	AGG	GTG	GCC	GAA	TCA	ACT	TAC	CAG	CAC	2610
H	P	K	R	P	S	R	Q	I	H	K	G	D	I	T	L	V	P	T	I	765
CAC	CCA	AAA	AGG	CCA	TCC	CGG	CAG	ATT	CAC	AAA	GGG	GAC	ATC	ACA	TTG	GTG	CCT	ACC	ATA	2670
N	G	T	L	P	I	R	S	H	H	R	S	S	P	S	S	S	P	T	L	785
AAT	GGC	ACT	CTG	CCC	ATC	AGA	TCT	CAT	CAC	AGA	TCG	TCT	CCA	TCT	TCA	TCT	CCT	ACC	TTA	2730
E	R	G	Q	M	G	S	R	Q	S	H	N	S	H	Q	S	L	N	S	L	805
GAA	AGA	GGG	CAG	ATG	GGC	AGC	CGG	CAG	AGT	CAC	AAC	AGT	CAC	CAG	TCA	CTC	AAC	AGT	TTG	2790
V	T	I	S	S	N	H	V	P	E	N	F	S	L	E	L	T	H	A	T	825
GTG	ACA	ATC	TCA	TCA	AAC	CAC	GTG	CCA	GAG	AAT	TTC	TCA	TTA	GAA	CTC	ACC	CAC	GCC	ACT	2850
P	A	V	E	Q	V	S	Q	L	L	S	M	L	H	Q	G	Q	Y	Q	P	845
CCT	GCT	GTT	GAG	CAG	GTC	TCT	CAG	CTT	CTT	TCA	ATG	CTT	CAC	CAG	GGG	CAA	TAT	CAG	CCA	2910
R	P	S	F	R	G	N	K	Y	S	R	S	Y	R	Y	A	L	Q	D	M	865
AGA	CCA	AGT	TTT	CGA	GGA	AAC	AAA	TAT	TCC	AGG	AGC	TAC	AGA	TAT	GCC	CTT	CAA	GAC	ATG	2970
D	K	F	S	L	K	D	S	G	R	G	D	S	E	A	G	D	S	D	Y	885
GAC	AAA	TTT	AGC	TTG	AAA	GAC	AGT	GGC	CGT	GGT	GAC	AGT	GAG	GCA	GGA	GAC	AGT	GAT	TAT	3030

Fig. 1F

D	L	G	R	D	S	P	I	D	R	L	L	G	E	G	F	S	D	L	F	905
GAT	TTG	GGG	CGA	GAT	TCT	CCA	ATA	GAT	AGG	CTG	CTG	GGT	GAA	GGA	TTC	AGC	GAC	CTG	TTT	3090
L	T	D	G	R	I	P	A	A	M	R	L	C	T	E	E	C	R	V	L	925
CTC	ACA	GAT	GGA	AGA	ATT	CCA	GCA	GCT	ATG	AGA	CTC	TGC	ACG	GAG	GAG	TGC	AGG	GTC	CTG	3150
G	H	S	D	Q	C	W	M	P	P	L	P	S	P	S	S	D	Y	R	S	945
GGA	CAC	TCT	GAC	CAG	TGC	TGG	ATG	CCA	CCA	CTG	CCC	TCA	CCG	TCT	TCT	GAT	TAT	AGG	AGT	3210
N	M	F	I	P	G	E	E	F	P	T	Q	P	Q	Q	Q	H	P	H	Q	965
AAC	ATG	TTC	ATT	CCA	GGG	GAA	GAA	TTC	CCA	ACG	CAA	CCC	CAG	CAG	CAG	CAT	CCA	CAT	CAG	3270
S	L	E	D	D	A	Q	P	A	D	S	G	E	K	K	K	S	F	S	T	985
AGT	CTT	GAG	GAT	GAC	GCT	CAG	CCT	GCA	GAT	TCC	GGT	GAA	AAG	AAG	AAG	AGT	TTT	TCC	ACC	3330
F	G	K	D	S	P	N	D	E	D	T	G	D	T	S	T	S	S	L	L	1005
TTT	GGA	AAG	GAC	TCC	CCA	AAC	GAT	GAG	GAC	ACT	GGG	GAT	ACC	AGC	ACA	TCA	TCT	CTG	CTC	3390
S	E	M	S	S	V	F	Q	R	L	L	P	P	S	L	D	T	Y	S	E	1025
TCG	GAA	ATG	AGC	AGT	GTG	TTT	CAG	CGT	CTC	TTA	CCG	CCT	TCC	CTG	GAC	ACC	TAT	TCT	GAA	3450
C	S	E	V	D	R	S	N	S	L	E	R	R	K	G	P	L	P	A	K	1045
TGC	AGT	GAG	GTG	GAT	CGG	TCC	AAC	TCC	CTG	GAG	CGC	AGG	AAG	GGA	CCC	TTG	CCA	GCC	AAA	3510

Fig. 1G

T	V	G	G	Y	P	Q	G	V	A	A	W	A	A	S	T	H	F	Q	N	P	1065
ACT	GTG	GGT	TAC	CCA	CAG	CAG	GGG	GTA	GCG	GCA	TGG	GCA	GCC	AGT	ACG	CAT	TTT	CAA	AAT	CCC	3570
T	T	N	C	G	P	P	L	L	G	T	H	S	S	V	Q	P	S	S	K	W	1085
ACC	ACC	AAC	TGT	GGG	CCG	CCA	CTT	GGA	ACT	CAC	TCC	AGT	AGT	GTG	CAG	CCT	TCT	TCA	AAA	TGG	3630
L	P	A	M	E	E	I	P	E	N	Y	E	E	D	D	F	D	N	V	L	L	1105
CTG	CCA	GCC	ATG	GAG	GAG	ATC	CCT	GAA	AAT	TAT	GAG	GAA	GAT	GAT	GAT	TTT	GAC	AAT	GTG	CTC	3690
N	H	L	N	D	G	K	H	E	L	M	D	A	S	E	L	V	A	E	I	I	1125
AAC	CAC	CTC	AAT	GAT	GGG	AAA	CAC	GAA	CTC	ATG	GAT	GCC	AGT	AGT	GAA	CTG	GTG	GCA	GAG	ATT	3750
N	K	L	L	Q	D	V	R	Q	S	*											1135
AAC	AAA	CTG	CTT	CAA	GAT	GTC	CGC	CAG	AGC	TAG											3783
GAG	ATTTAG	CGAAG	CAATTTT	TGTTTCC	ATGTATAT	TGGAAATAG	GGAACAACAACA	CAACAAACCA	CAACCAACCA	CAACCAACCA	CAACCAACCA	CAACCAACCA	CAACCAACCA	CAACCAACCA	CAACCAACCA	CAACCAACCA	CAACCAACCA	CAACCAACCA	CAACCAACCA	CAACCAACCA	3862
TGG	CATTG	CCAAA	TAGTTG	CAATTTAT	CAATAAATG	TCTGTATAT	TGTAATTA	GAATTA	GAATTA	GAATTA	GAATTA	GAATTA	GAATTA	GAATTA	GAATTA	GAATTA	GAATTA	GAATTA	GAATTA	GAATTA	3941
CAATG	CAAGT	GTGATT	TTTAA	CTGTATTT	TAAATCTG	TATTTTAA	AAATACATTT	TGTACCTT	TATATTT	TATATTT	TATATTT	TATATTT	TATATTT	TATATTT	TATATTT	TATATTT	TATATTT	TATATTT	TATATTT	TATATTT	4020
TTTTAT	TTTTT	ACTCC	CAATG	ACATG	TTTTC	CTAGT	CGTAG	AACTAG	CCACTG	TCAAA	TCTG	ATAC	ACTA	4099							
TTCA	ACCACA	AGTGT	AAAGC	ACTG	CTTAG	ATTAG	TTTGT	TGGGA	AGAA	TTATT	ATG	TGT	ATG	AAAC	ACCC	CACT	4178				
GAAG	CATTAT	ACAATT	CTTA	ATTC	CAATTA	AGTGA	TCCACT	TTTTT	TCAATA	ACTTTT	TAGAAA	TTAA	GAAT	CA	TTAA	4257					
ATTG	TTAAG	CTATTT	TATTT	ATTT	CTCT	ACTTT	CTACT	AGCC	CAATAG	TTGA	CTCT	TATAG	GGAAA	ATCG	AAAAG	4336					
TAAAG	TGAAAG	TTTATTT	CAGG	ACTG	AGAA	TATCTT	GAGG	TTATTT	TATAG	ATG	ACTAT	CTCA	AA	TGA	ACTTTT	TAT	4415				

Fig. 1H

AGACAAATGATGAAACAGAACTAAAGTCAATGTTTCCCTGACTCCCAGGCCCCCTACTATTCCAGGCCATCACACTGGCCT 4494
 GTTCCGGAGAAATATTTCTCTCACAAATATATATCTACTTATAATATGGTAAACAATAAAATTTTATTCCATCCTTGTA 4573
 GTATGAAACATGCTCCAGGAAATGGAATCTGTCCCTTAAATGGATAACAGTATGTGTTCTAAATGGCATAAAAATATTAC 4652
 TGGATAAAACAGTTGTGTGTCAGTGTCTCCTAAGGTAGTAAATAATAATTGACTTATTCTGAACCCATTCTATTTTGAA 4731
 TCTCCCCCTTCTCCATACATACTTGAACATTTTAATCTTTTGGAAATATTGTCTTTCTTTGTATAAATAATTCATTTT 4810
 AGCTTTTGTCTCCAGTGCAATGATCTCATATTTTGTCTTTTATTTTAGTATAAGAACATTTATATAAAATCATATTTTGT 4889
 TACTGCAATTTGTTTATTTGTTGTGGCAAAATGAGAAATCCCTTTATTTATTTGTGCTGTGATCTCTCTGTGGAAATGC 4968
 CTTGGTGAGAGAGATGCTTATTATGACTATTATCATTTCTGACCAAGCTTCTATTAAATGTTATTCTTAATAATACACTA 5047
 TCTTGATTGTACTCTCCAGAAAAATTTTCTGTCTCAGTGAAAAATAAAGAAAAATTAAGTAAAAAATTAAGTAAAAA 5121

Fig. 11

I	E	F	D	V	I	T	L	P	T	E	H	L	Q	L	F	H	I	E	V	125
ATA	GAG	TTT	GAT	GTG	ATC	ACT	CTA	CCC	ACA	GAG	CAT	CTG	CAG	CTT	TTC	CAT	ATT	GAA	GTT	750
E	V	L	D	I	N	D	N	S	P	Q	F	S	R	S	L	I	P	I	E	145
GAA	GTG	CTG	GAT	ATT	AAT	GAC	AAT	TCT	CCC	CAG	TTT	TCA	AGA	TCT	CTC	ATA	CCT	ATT	GAG	810
I	S	E	S	A	A	V	G	T	R	I	P	L	D	S	A	F	D	P	D	165
ATA	TCT	GAG	AGT	GCA	GCA	GTT	GGG	ACT	CGC	ATT	CCC	CTG	GAC	AGT	GCA	TTT	GAT	CCA	GAT	870
V	G	E	N	S	L	H	T	Y	S	L	S	A	N	D	F	F	N	I	E	185
GTT	GGG	GAA	AAT	TCC	CTC	CAC	ACA	TAC	TCG	CTC	TCT	GCC	AAT	GAT	TTT	TTT	AAT	ATC	GAG	930
V	R	T	R	T	D	G	A	K	Y	A	E	L	I	V	V	R	E	L	D	205
GTT	CGG	ACC	AGG	ACT	GAT	GGA	GCC	AAG	TAT	GCA	GAA	CTC	ATA	GTG	GTC	AGA	GAG	TTA	GAT	990
R	E	L	K	S	S	Y	E	L	Q	L	T	A	S	D	M	G	V	P	Q	225
CGG	GAG	CTG	AAG	TCA	AGC	TAC	GAG	CTT	CAG	CTC	ACT	GCC	TCA	GAC	ATG	GGA	GTA	CCT	CAG	1050
R	S	G	S	S	I	L	K	I	S	I	S	D	S	N	D	N	S	P	A	245
AGG	TCT	GGC	TCA	TCC	ATA	CTA	AAA	ATA	AGC	ATT	TCA	GAC	TCC	AAT	GAC	AAC	AGC	CCT	GCT	1110
F	E	Q	Q	S	Y	I	I	Q	L	L	E	N	S	P	V	G	T	L	L	265
TTT	GAG	CAG	CAA	TCT	TAT	ATA	ATA	CAA	CTC	TTA	GAA	AAC	TCC	CCG	GTT	GGC	ACT	TTG	CTC	1170

Fig. 2B

L	D	L	L	N	A	T	D	P	D	E	G	A	N	G	K	I	V	Y	S	F	285	
TTA	GAT	CTG	AAT	GCC	ACG	GAT	CCA	GAT	CCA	GAT	GAG	GCG	GCT	AAT	GGG	AAA	ATT	GTA	TAT	TCC	TTC	1230
S	S	H	V	S	P	K	I	M	E	E	T	F	K	I	D	S	E	R	G	H	305	
AGC	AGT	CAT	GTG	TCT	CCC	AAA	ATT	ATG	GAG	ACT	TTT	AAA	ATT	GAT	TCT	GAA	AGA	GGA	CAT	1290		
L	T	L	F	K	Q	V	D	Y	E	I	T	K	S	Y	E	I	D	V	Q	325		
TTG	ACT	CTT	TTC	AAG	CAA	GTG	GAT	TAT	GAA	ATC	ACC	AAA	TCC	TAT	GAG	ATT	GAT	GTT	CAG	1350		
A	Q	D	L	G	P	N	S	I	P	A	H	C	K	I	I	I	K	V	V	345		
GCT	CAA	GAT	TTG	GGT	CCA	AAT	TCA	ATC	CCA	GCC	CAT	TGC	AAA	ATT	ATA	ATT	AAG	GTT	GTG	1410		
D	V	N	D	N	K	P	E	I	N	I	N	L	M	S	P	G	K	E	E	365		
GAT	GTT	AAT	GAC	AAT	AAA	CCT	GAA	ATT	AAC	ATC	AAC	CTC	ATG	TCC	CCT	GGA	AAA	GAA	GAA	1470		
I	S	Y	I	F	E	G	D	P	I	D	T	F	V	A	L	V	R	V	Q	385		
ATA	TCT	TAT	ATT	TTT	GAA	GGG	GAT	CCT	ATT	GAT	ACA	TTT	GTT	GCT	TTG	GTC	AGA	GTT	CAG	1530		
D	K	D	S	G	L	N	G	E	I	V	C	K	L	H	G	H	G	H	F	405		
GAC	AAG	GAT	TCT	GGG	CTG	AAT	GGA	GAA	ATA	GTT	TGT	AAG	CTT	CAT	GGA	CAT	GGT	CAC	TTT	1590		
K	L	Q	K	T	Y	E	N	N	Y	L	I	L	T	N	A	T	L	D	R	425		
AAA	CTT	CAG	AAG	ACA	TAT	GAA	AAC	AAT	TAT	TTA	ATC	TTA	ACT	AAT	GCC	ACA	CTG	GAT	AGA	1650		

Fig. 2C

E	K	R	S	E	Y	S	L	T	V	I	A	E	D	R	G	T	P	S	L	445
GAA	AAG	AGA	TCT	GAG	TAT	AGT	TTG	ACT	GTA	ATC	GCT	GAG	GAC	AGG	GGG	ACA	CCC	AGT	CTC	1710
S	T	V	K	H	F	T	V	Q	I	N	D	I	N	D	N	P	P	H	F	465
TCT	ACA	GTG	AAA	CAT	TTT	ACA	GTT	CAA	ATC	AAT	GAT	ATC	AAT	GAC	AAT	CCA	CCC	CAC	TTC	1770
Q	R	S	R	Y	E	F	V	I	S	E	N	N	S	P	G	A	Y	I	T	485
CAG	AGA	AGC	CGA	TAT	GAA	TTT	GTA	ATT	TCA	GAA	AAT	AAC	TCA	CCA	GGG	GCA	TAT	ATC	ACC	1830
T	V	T	A	T	D	P	D	L	G	E	N	G	Q	V	T	Y	T	I	L	505
ACT	GTT	ACA	GCC	ACA	GAT	CCT	GAT	CTT	GGA	GAA	AAT	GGG	CAA	GTG	ACA	TAC	ACC	ATC	TTG	1890
E	S	F	I	L	G	S	S	I	T	T	Y	V	T	I	D	P	S	N	G	525
GAG	AGT	TTT	ATT	CTA	GGA	AGT	TCC	ATA	ACT	ACA	TAT	GTA	ACC	ATT	GAC	CCA	TCT	AAT	GGA	1950
A	I	Y	A	L	R	I	F	D	H	E	E	V	S	Q	I	T	F	V	V	545
GCC	ATC	TAT	GCC	CTC	AGA	ATC	TTT	GAT	CAT	GAA	GAA	GTG	AGT	CAG	ATC	ACT	TTT	GTG	GTA	2010
E	A	R	D	G	G	S	P	K	Q	L	V	S	N	T	T	V	V	L	T	565
GAA	GCA	AGA	GAT	GGA	GGA	AGC	CCG	AAG	CAA	CTG	GTA	AGC	AAT	ACC	ACA	GTT	GTG	CTC	ACC	2070
I	I	D	E	N	D	N	V	P	V	V	I	G	P	A	L	R	N	N	T	585
ATC	ATT	GAC	GAA	AAT	GAC	AAC	GTT	CCT	GTG	GTT	ATA	GGG	CCT	GCA	TTG	CGT	AAT	AAT	ACG	2130

Fig. 2D

A	E	I	T	I	P	K	G	A	E	S	G	F	H	V	T	R	I	R	A	605
GCA	GAA	ATC	ACC	ATT	CCC	AAA	GGG	GCT	GAA	AGT	GGC	TTT	CAT	GTC	ACA	AGA	ATA	AGG	GCA	2190
I	D	R	D	S	G	V	N	A	E	L	S	C	A	I	V	A	G	N	E	625
ATT	GAC	AGA	GAC	TCT	GGT	GTG	AAT	GCT	GAA	CTC	AGC	TGC	GCC	ATA	GTA	GCA	GGT	AAT	GAG	2250
E	N	I	F	I	I	D	P	R	S	C	D	I	H	T	N	V	S	M	D	645
GAG	AAT	ATC	TTC	ATA	ATT	GAT	CCA	CGA	TCA	TGT	GAC	ATC	CAT	ACC	AAC	GTT	AGC	ATG	GAT	2310
S	V	P	Y	T	E	W	E	L	S	V	I	I	Q	D	K	G	N	P	Q	665
TCT	GTT	CCC	TAC	ACA	GAA	TGG	GAG	CTG	TCA	GTT	ATC	ATT	CAG	GAC	AAA	GGC	AAT	CCT	CAG	2370
L	H	T	K	V	L	L	K	C	M	I	F	E	Y	A	E	S	V	T	S	685
CTA	CAT	ACC	AAA	GTC	CTT	CTG	AAG	TGC	ATG	ATC	TTT	GAA	TAT	GCA	GAG	TCG	GTG	ACA	AGT	2430
T	A	M	T	S	V	S	Q	A	S	L	D	V	S	M	I	I	I	I	S	705
ACA	GCA	ATG	ACT	TCA	GTA	AGC	CAG	GCA	TCC	TTG	GAT	GTC	TCC	ATG	ATA	ATA	ATT	ATT	TCC	2490
L	G	A	I	C	A	V	L	L	V	I	M	V	L	F	A	T	R	C	N	725
TTA	GGA	GCA	ATT	TGT	GCA	GTG	TTG	CTG	GTT	ATT	ATG	GTG	CTA	TTT	GCA	ACT	AGG	TGT	AAC	2550
R	E	K	K	D	T	R	S	Y	N	C	R	V	A	E	S	T	Y	Q	H	745
CGC	GAG	AAG	AAA	GAC	ACT	AGA	TCC	TAT	AAC	TGC	AGG	GTG	GCC	GAA	TCA	ACT	TAC	CAG	CAC	2610

Fig. 2E

H	P	K	R	P	S	R	Q	I	H	K	G	D	I	T	L	V	P	T	I	765
CAC	CCA	AAA	AGG	CCA	TCC	CGG	CAG	ATT	CAC	AAA	GGG	GAC	ATC	ACA	TTG	GTG	CCT	ACC	ATA	2670
N	G	T	L	P	I	R	S	H	H	R	S	S	P	S	S	S	P	T	L	785
AAT	GGC	ACT	CTG	CCC	ATC	AGA	TCT	CAT	CAC	AGA	TCG	TCT	CCA	TCT	TCA	TCT	CCT	ACC	TTA	2730
E	R	G	Q	M	G	S	R	Q	S	H	N	S	H	Q	S	L	N	S	L	805
GAA	AGA	GGG	CAG	ATG	GGC	AGC	CGG	CAG	AGT	CAC	AAC	AGT	CAC	CAG	TCA	CTC	AAC	AGT	TTG	2790
V	T	I	S	S	N	H	V	P	E	N	F	S	L	E	L	T	H	A	T	825
GTG	ACA	ATC	TCA	TCA	AAC	CAC	GTG	CCA	GAG	AAT	TTC	TCA	TTA	GAA	CTC	ACC	CAC	GCC	ACT	2850
P	A	V	E	V	S	Q	L	L	S	M	L	H	Q	G	Q	Y	Q	P		844
CCT	GCT	GTT	GAG	GTC	TCT	CAG	CTT	CTT	TCA	ATG	CTT	CAC	CAG	GGG	CAA	TAT	CAG	CCA		2907
R	P	S	F	R	G	N	K	Y	S	R	S	Y	R	Y	A	L	Q	D	M	864
AGA	CCA	AGT	TTT	CGA	GGA	AAC	AAA	TAT	TCC	AGG	AGC	TAC	AGA	TAT	GCC	CTT	CAA	GAC	ATG	2967
D	K	F	S	L	K	D	S	G	R	G	D	S	E	A	G	D	S	D	Y	884
GAC	AAA	TTT	AGC	TTG	AAA	GAC	AGT	GGC	CGT	GGT	GAC	AGT	GAG	GCA	GGA	GAC	AGT	GAT	TAT	3027
D	L	G	R	D	S	P	I	D	R	L	L	G	E	G	F	S	D	L	F	904
GAT	TTG	GGG	CGA	GAT	TCT	CCA	ATA	GAT	AGG	CTG	CTG	GGT	GAA	GGA	TTC	AGC	GAC	CTG	TTT	3087

Fig. 2F

L	T	D	G	R	I	P	A	A	M	R	L	C	T	E	E	C	R	V	L	924
CTC	ACA	GAT	GGA	AGA	ATT	CCA	GCA	GCT	ATG	AGA	CTC	TGC	ACG	GAG	GAG	TGC	AGG	GTC	CTG	3147
G	H	S	D	Q	C	W	M	P	P	L	P	S	P	S	S	D	Y	R	S	944
GGA	CAC	TCT	GAC	CAG	TGC	TGG	ATG	CCA	CCA	CTG	CCC	TCA	CCG	TCT	TCT	GAT	TAT	AGG	AGT	3207
N	M	F	I	P	G	E	E	F	P	T	Q	P	Q	Q	Q	H	P	H	Q	964
AAC	ATG	TTC	ATT	CCA	GGG	GAA	GAA	TTC	CCA	ACG	CAA	CCC	CAG	CAG	CAG	CAT	CCA	CAT	CAG	3267
S	L	E	D	D	A	Q	P	A	D	S	G	E	K	K	K	S	F	S	T	984
AGT	CTT	GAG	GAT	GAC	GCT	CAG	CCT	GCA	GAT	TCC	GGT	GAA	AAG	AAG	AAG	AGT	TTT	TCC	ACC	3327
F	G	K	D	S	P	N	D	E	D	T	G	D	T	S	T	S	S	L	L	1004
TTT	GGA	AAG	GAC	TCC	CCA	AAC	GAT	GAG	GAC	ACT	GGG	GAT	ACC	AGC	ACA	TCA	TCT	CTG	CTC	3387
S	E	M	S	S	V	F	Q	R	L	L	P	P	S	S	L	D	T	Y	S	1024
TCG	GAA	ATG	AGC	AGT	GTG	TTC	CAG	CGT	CTC	TTA	CCG	CCT	TCC	CTG	GAC	ACC	TAT	TCT	GAA	3447
C	S	E	V	D	R	S	N	S	L	E	R	R	K	G	P	L	P	A	K	1044
TGC	AGT	GAG	GTG	GAT	CGG	TCC	AAC	TCC	CTG	GAG	CGC	AGG	AAG	GGA	CCC	TTG	CCA	GCC	AAA	3507
T	V	G	Y	P	Q	G	V	A	A	W	A	A	S	T	H	F	Q	N	P	1064
ACT	GTG	GGT	TAC	CCA	CAG	GGG	GTA	GCG	GCA	TGG	GCA	GCC	AGT	ACG	CAT	TTT	CAA	AAT	CCC	3567

Fig. 2G

T	T	N	C	G	P	P	L	G	T	H	S	S	V	Q	P	S	S	K	W	1084
ACC	ACC	AAC	TGT	GGG	CCG	CCA	CTT	GGA	ACT	CAC	TCC	AGT	GTG	CAG	CCT	TCT	TCA	AAA	TGG	3627
L	P	A	M	E	E	I	P	E	N	Y	E	E	D	D	F	D	N	V	L	1104
CTG	CCA	GCC	ATG	GAG	GAG	ATC	CCT	GAA	AAT	TAT	GAG	GAA	GAT	GAT	TTT	GAC	AAT	GTG	CTC	3687
N	H	L	N	D	G	K	H	E	L	M	D	A	S	E	L	V	A	E	I	1124
AAC	CAC	CTC	AAT	GAT	GGG	AAA	CAC	GAA	CTC	ATG	GAT	GCC	AGT	GAA	CTG	GTG	GCA	GAG	ATT	3747
N	K	L	L	Q	D	V	R	Q	S	*										1134
AAC	AAA	CTG	CTT	CAA	GAT	GTC	CGC	CAG	AGC	TAG										3780
GAG	ATTTAG	CGAAG	CATTTT	TGTTTCC	ATGTATAT	GGAAATAG	GGAAACAACAACA	CAAAACCCCTG	AAAGAAC											3859
TGG	CAT	TGCC	AAATAG	TTCATTTAT	CATAAAATG	TCTGTATAT	TGAATATTA	ATACTGTAT	TTTCGTATGTACA											3938
CAATG	CAAGT	GTGAT	TATTTAATC	TGTAATTTTAA	AAATACATTTG	TACCTTATAT	TATTTATGT	ATAATTTAAC	AAACAAA											4017
TTTTAT	TTTTTT	ACTCC	ATGAC	AGACAT	GTGTTT	TCCTAG	TCGTAG	AAACTAG	CCACTGTTCAA	ATCTGATAC	ACTA									4096
TTCAAC	CACAAAG	TAAAGG	CACTGCT	TAGATTAG	TTTGT	TGGGAAG	AATATTAT	TGTTGATGA	ACAACCCCACT											4175
GAAGCA	TTATACA	ATTCTTA	ATTC	CAATTAAG	TGATCC	CACTTTT	TTCATTA	ACTTTT	TAGAAATTA	AGAATCAT	TAAA									4254
ATTGTT	AAGCTAT	TTTAT	TGTTAT	TTTCT	CTACTT	CTACTAG	CCCCAATAG	TTGAAC	TCTTATAG	GAAATCG	AAAGA									4333
TAAAGT	GAAAGTT	TATTT	CAGGAC	TGAGAA	TATCTT	GAGGTTAT	TATTA	TAGATG	ACTATCTCAA	ATGA	ACTTTT	TAT								4412
AGACAA	TGATGA	AAACAG	AACTAA	AGTCAAT	GTTTCC	TGACTCCC	AGCCCC	TACTAT	TCCAGGCC	ATCACAC	TGGCCT									4491
GTTC	CGGAGA	ATATTT	CTCTC	ACAAATAT	TATATCT	ACTTATA	ATTA	TGGTAA	CAATAA	ATTTTAT	TCCATC	CTTGTA								4570
GTATGA	AAACATG	CTCCA	AGGAAATG	GAATCTG	TCCCTT	TAAATG	GATAAC	AGTATG	TCTTAATG	GCATAA	ATATAC									4649
TGGATA	AAAAAC	AGTTGT	GTGTC	TCTCT	CTCCTA	AGGTAG	TAAATATA	ATTG	ACTTAT	TCTGA	ACCCAT	TCTTTGAA								4728

Fig. 2H

TCTCCCCTTTCCCTCTCACAAATACCTTGAACATTTTAAATCCTTTTGGAAATATTGTCCTTTCTTTTGGTTATAAACTATTTCATTTT 4807
AGCTTTTGTCTCCAGTGCATGATCTCATATTTTGTGCTTTTATTTTAGTATAAGAACATTTTATATAAAATCATATTTTGT 4886
TACTGCAATTGTTTATTGTTGTGGCAAAATGAGAAATCCCTTTATTATTGCTGTGATCTCTCTGTGGAATGC 4965
CTTGGTGAGAGAGATGCTTATTATGACTATTATCATTTCTGACCAAGCTTCTATTAAATGTTATTCTTAATAATACACTA 5044
TCTTGATTGTACTCTCCAGAAAATTTTCTGTCTCAGTGAAAAATAAAGAAAAATTTAAAGTAAAAAATAAAAAA 5118

Fig. 2I

T416	1651	GAAAAGAGATCTGAGTATAGTTTGGACTGTAATCGCTGAGGACAGGGGGAC	1700
AL137471	1	...AAGAGATCTGAGTATAGTTTGGACTGTAATCGCTGAGGACAGGGGGAC	47
T416	1701	ACCCAGTCTCTTACAGTGAAACATTTTACAGTTCAAATCAATGATATCA	1750
AL137471	48	ACCCAGTCTCTTACAGTGAAACATTTTACAGTTCAAATCAATGATATCA	97
T416	1751	ATGACAATCCACCCCACTTCCAGAGAAAGCCGATATGAATTTGTAATTCA	1800
AL137471	98	ATGACAATCCACCCCACTTCCAGAGAAAGCCGATATGAATTTGTAATTCA	147
T416	1801	GAAAATAACTCACCCAGGGGCATATATCACCACTGTTACAGCCACAGATCC	1850
AL137471	148	GAAAATAACTCACCCAGGGGCATATATCACCACTGTTACAGCCACAGATCC	197
T416	1851	TGATCTTGGAGAAAATGGGCAAGTGACATACACCATCTTGGAGAGTTTA	1900
AL137471	198	TGATCTTGGAGAAAATGGGCAAGTGACATACACCATCTTGGAGAGTTTA	247
T416	1901	TTCTAGGAAAGTTCCATAAATACTACATATGTAAACCATTGACCCCATCTAATGGA	1950
AL137471	248	TTCTAGGAAAGTTCCATAAATACTACATATGTAAACCATTGACCCCATCTAATGGA	297

FIG. 4A

T416	1951	GCCATCTATGCCCTCAGAAATCTTTGATCATGAAGAAGTGAGTCAGATCAC	2000
AL137471	298	GCCATCTATGCCCTCAGAAATCTTTGATCATGAAGAAGTGAGTCAGATCAC	347
T416	2001	TTTTGTGGTAGAAGCAAGAGATGGAGGAAGCCCCGAAGCAACTGGTAAGCA	2050
AL137471	348	TTTTGTGGTAGAAGCAAGAGATGGAGGAAGCCCCGAAGCAACTGGTAAGCA	397
T416	2051	ATACCACAGTTGTGCTCACCATCATTTGACGAAATGACAACGTTCCCTGTG	2100
AL137471	398	ATACCACAGTTGTGCTCACCATCATTTGACGAAATGACAACGTTCCCTGTG	447
T416	2101	GTTATAGGGCCCTGCATTGCGTAATAATACGGCAGAAATCACCATTTCCCAA	2150
AL137471	448	GTTATAGGGCCCTGCATTGCGTAATAATACGGCAGAAATCACCATTTCCCAA	497
T416	2151	AGGGGCTGAAAGTGGCTTTCATGTCAACAAGATAAGGGCAATTGACAGAG	2200
AL137471	498	AGGGGCTGAAAGTGGCTTTCATGTCAACAAGATAAGGGCAATTGACAGAG	547
T416	2201	ACTCTGGTGTGAATGCTGAACCTCAGCTGCGCCCATAGTAGCAGGTAATGAG	2250
AL137471	548	ACTCTGGTGTGAATGCTGAACCTCAGCTGCGCCCATAGTAGCAGGTAATGAG	597

FIG. 4B

T416	2251	GAGAAATATCTT	CATAAATTGATCCACGATCATGTGACATCCATACCAACGT	2300
AL137471	598	GAGAAATATCTT	CATAAATTGATCCACGATCATGTGACATCCATACCAACGT	647
T416	2301	TAGCATGGATTCT	GTTCCCTACACAGAAATGGGAGCTGTCAGTTATCATTC	2350
AL137471	648	TAGCATGGATTCT	GTTCCCTACACAGAAATGGGAGCTGTCAGTTATCATTC	697
T416	2351	AGGACAAAAGGCAAT	CCTCAGCTACATACCAAAGTCCTTCTGAAGTGCATG	2400
AL137471	698	AGGACAAAAGGCAAT	CCTCAGCTACATACCAAAGTCCTTCTGAAGTGCATG	747
T416	2401	ATCTTTGAAATATG	CAGAGTCGGTGACAAAGTACAGCAATGACTTCAGTAAG	2450
AL137471	748	ATCTTTGAAATATG	CAGAGTCGGTGACAAAGTACAGCAATGACTTCAGTAAG	797
T416	2451	CCAGGCATCCTTGG	ATGTCCTCCATGATAATAATTATTTCCTTAGGAGCAA	2500
AL137471	798	CCAGGCATCCTTGG	ATGTCCTCCATGATAATAATTATTTCCTTAGGAGCAA	847
T416	2501	TTTGTGCAGTGTG	CTGGTTATTATGGTGCTATTTTGCAACTAGGTGTAAC	2550
AL137471	848	TTTGTGCAGTGTG	CTGGTTATTATGGTGCTATTTTGCAACTAGGTGTAAC	897

FIG. 4C

T416	2551	CGCGAGAAAGAAAGACACTAGATCCTATACTGACGGTGGCCGAATCAAC	2600
AL137471	898	CGCGAGAAAGAAAGACACTAGATCCTATACTGACGGTGGCCGAATCAAC	947
T416	2601	TTACCAGCACCCACCCAAAAGGCCATCCCGGCAGATTTCACAAAAGGGGACA	2650
AL137471	948	TTACCAGCACCCACCCAAAAGGCCATCCCGGCAGATTTCACAAAAGGGGACA	997
T416	2651	TCACATTGGTGCCCTACCATAAATGGCACTCTGCCCATCAGATCTCATCAC	2700
AL137471	998	TCACATTGGTGCCCTACCATAAATGGCACTCTGCCCATCAGATCTCATCAC	1047
T416	2701	AGATCGTCTCCATCTTCAATCTCCTACCTTAGAAAAGAGGGCAGATGGGCAG	2750
AL137471	1048	AGATCGTCTCCATCTTCAATCTCCTACCTTAGAAAAGAGGGCAGATGGGCAG	1097
T416	2751	CCGGCAGAGTCACAACAGTCAACAGTCACTCAACAGTTTGGTGACAAATCT	2800
AL137471	1098	CCGGCAGAGTCACAACAGTCAACAGTCACTCAACAGTTTGGTGACAAATCT	1147
T416	2801	CATCAAACACGTGCCAGAGAAATTCTCTATTAGAACTCACCCACGCCACT	2850
AL137471	1148	CATCAAACACGTGCCAGAGAAATTCTCTATTAGAACTCACCCACGCCACT	1197

FIG. 4D

T416	2851	CCTGCTGTGAGCAGGTCCTCTCAGCTTCTTTCAATGCTTCACCAGGGCA	2900
AL137471	1198	CCTGCTGTGAGCAGGTCCTCTCAGCTTCTTTCAATGCTTCACCAGGGCA	1247
T416	2901	ATATCAGCCAAAGACCAAGTTTTCGAGGAAACAAATATTCCAGGAGCTACA	2950
AL137471	1248	ATATCAGCCAAAGACCAAGTTTTCGAGGAAACAAATATTCCAGGAGCTACA	1297
T416	2951	GATATGCCCTTCAAGACATGGACAAATTTAGCTTGAAAGACAGTGCCCGT	3000
AL137471	1298	GATATGCCCTTCAAGACATGGACAAATTTAGCTTGAAAGACAGTGCCCGT	1347
T416	3001	GGTGACAGTGAGGCAGGACAGTGATTATGATTGGGGCCGAGATTCTCC	3050
AL137471	1348	GGTGACAGTGAGGCAGGACAGTGATTATGATTGGGGCCGAGATTCTCC	1397
T416	3051	AATAGATAGGCTGCTGGGTGAAGATTTCAGCGACCTGTTTCTCACAGATG	3100
AL137471	1398	AATAGATAGGCTGTTGGGTGAAGATTTCAGCGACCTGTTTCTCACAGATG	1447
T416	3101	GAAGAAATTCAGCAGCTATGAGACTCTGCACGGAGGAGTGCAGGGTCCTG	3150
AL137471	1448	GAAGAAATTCAGCAGCTATGAGACTCTGCACGGAGGAGTGCAGGGTCCTG	1497

FIG. 4E

T416	3151	GGACACTCTGACCAGTCTGGATGCCACCACTGCCCTCACCGTCTTCTGA	3200
AL137471	1498	GGACACTCTGACCAGTCTGGATGCCACCACTGCCCTCACCGTCTTCTGA	1547
T416	3201	TTATAGGAGTAACATGTTTCATTCCAGGGGAAGAAATTCCCAACGCAACCCC	3250
AL137471	1548	TTATAGGAGTAACATGTTTCATTCCAGGGGAAGAAATTCCCAACGCAACCCC	1597
T416	3251	AGCAGCAGCATCCACATCAGAGTCTTGAGGATGACGCTCAGCCTGCAGAT	3300
AL137471	1598	AGCAGCAGCATCCACATCAGAGTCTTGAGGATGACGCTCAGCCTGCAGAT	1647
T416	3301	TCCGGTGAAAAGAAAGAGTTTTTCCACCTTTGGAAAGGACTCCCCAAA	3350
AL137471	1648	TCCGGTGAAAAGAAAGAGTTTTTCCACCTTTGGAAAGGACTCCCCAAA	1697
T416	3351	CGATGAGGACACTGGGGATACCAGCACATCATCTCTGCTCTCGGAAATGA	3400
AL137471	1698	CGATGAGGACACTGGGGATACCAGCACATCATCTCTGCTCTCGGAAATGA	1747
T416	3401	GCA GTGTGTTCCAGCGTCTCTTACCGCCCTTCCCTGGACACCTATTCTGAA	3450
AL137471	1748	GCA GTGTGTTCCAGCGTCTCTTACCGCCCTTCCCTGGACACCTATTCTGAA	1797

FIG. 4F

T416	3451	TGCAGTGAGGTGGATCGGTCCAACTCCCTGGAGCGCAGGAAGGACCC	TT	3500	
AL137471	1798	TGCAGTGAGGTGGATCGGTCCAACTCCCTGGAGCGCAGGAAGGACCC	TT	1847	
T416	3501	GCCAGCCAAAAC	TGTGGGT	TACCCACAGGGGTAGCGGCATGGGCAGCCA	3550
AL137471	1848	GCCAGCCAAAAC	TGTGGGT	TACCCACAGGGGTAGCGGCATGGGCAGCCA	1897
T416	3551	GTACGCATTTTCAAAATCCCA	CACCAACTGTGGCCGCCACTT	TGGA	ACT 3600
AL137471	1898	GTACGCATTTTCAAAATCCCA	CACCAACTGTGGCCGCCACTT	TGGA	ACT 1947
T416	3601	CAC	TCCAGTGTGCAGCCTTCTTCAAAATGGCTGCCAGCCATGGAGGAGAT	3650	
AL137471	1948	CAC	TCCAGTGTGCAGCCTTCTTCAAAATGGCTGCCAGCCATGGAGGAGAT	1997	
T416	3651	CCCTGAAAAT	TATGAGGAAGATGATTTTGACAAATGTGCTCAACCACCTCA	3700	
AL137471	1998	CCCTGAAAAT	TATGAGGAAGATGATTTTGACAAATGTGCTCAACCACCTCA	2047	
T416	3701	ATGATGGGAAACACGAACTCATGGATGCCAGTGAAC	TGGTGGCAGAGATT	3750	
AL137471	2048	ATGATGGGAAACACGAACTCATGGATGCCAGTGAAC	TGGTGGCAGAGATT	2097	

FIG. 4G

T416	3751	AACA	AACTGCTTCAAGATGTCCGCCAGAGCTAGGAGATTTTAGCGAAGCA	3800
AL137471	2098	AACA	AACTGCTTCAAGATGTCCGCCAGAGCTAGGAGATTTTAGCGAAGCA	2147
T416	3801	TTTT	TGTTCCATGTATATGGAAATAGGGAACAACAACAACAAAAA	3850
AL137471	2148	TTTT	TGTTCCATGTATATGGAAATAGGGAACAACAACAACAAAAA	2197
T416	3851	CCCT	GAAAGAACTGGCATTGCCAAATAGTTGCATTTATCATAAATGTGTC	3900
AL137471	2198	CCCT	GAAAGAACTGGCATTGCCAAATAGTTGCATTTATCATAAATGTGTC	2247
T416	3901	TGTG	TATATTGAATATTAAATACTGTATTTTCGTATGTACACAAATGCAAG	3950
AL137471	2248	TGTG	TATATTGAATATTAAATACTGTATTTTCGTATGTACACACAAAAA	2297
T416	3951	TGTG	ATTATTTTAAATCTGTATTTTAAATAACATTTGTACCTTATATTTA	4000
AL137471	2298	AAAA	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAG.....	2338

FIG. 4H

T416	1	...	ATGCACCAAATG...	AATGCTAAAAATGCAC	TTTAGGTTTGT	TTT	TGCA	45
m-PC	1	ATGATGCTACTTCTG	CCCATTCCTGCTAGG	GCTCTTAGGGCCAGGA	AGCTA			50
T416	46	CTTCTGATAGTATCTT	CAACCAACGATGTA	CTGGCA...	AGAATTTGAA			92
m-PC	51	CT..TGTTCA	TTTCAGGGGATTGTCAGG	AGGTGGCCACTGT	CATGGTGAA			98
T416	93	ATACAGGATTTATGAG	GAACAGAGGGTTGGAT	CAGTAATTGCA	AAGACTAT			142
m-PC	99	ATTCCAAGTGACAGAG	GAAGTGCCGCTCTGGC	ACGGTGATAGG	GAAACTGT			148
T416	143	CAGAGGATGTGGCTGAT	GTTTTATTGAAGCTT	CCTAATCCTTCT	ACTGTT			192
m-PC	149	CCCAAGAACT..AGA.	GTGGAGGAGAGGCGT	GGGAAGGCAGG	AGATG..			193
T416	193	CGATTTTCGAGCCATG	CAGAGGGGAAATTCT	CCTCTACTTGT	AGTAAACGA			242
m-PC	194	CCTTCCAGATTCTGC	AGCTGCCCTCAGGCA	CTGCCGTT	CAGATGA	ACTC		242

FIG. 5A

T416	243	GGATAATGGGAAATCAGCATAGGGCTACAATTGACCGTGAACAAC	292
m-PC	243	TGAGACGGCCTGCTCAGCACTTCCAGCCGGCTGGATCGGGAAGCTAT	292
T416	293	GCCAGAAAACTTGAACCTGTTCATAGAGTTTGATGTGATCACTCTACCC	342
m-PC	293	GTCGGCAGGAAGATCCCCTGTCTGTGTGCATTTGACGTG.....CTTGCC	336
T416	343	ACA.GAGCATCTGCAGCTTTTCCATATTGAAGTTGAAGTGCTGGATATTA	391
m-PC	337	ACAGGGCGTCTGC.TCTAATTCAATGTGGAGATTCAGGTGCTAGACATCA	385
T416	392	ATGACAAATCTCCCCAGTTTTCAGATCTCTCATACCTATTGAGATATCT	441
m-PC	386	ATGACCACCCAGCCACAGTTTCCCCAAAGACGACGGAAC	435
T416	442	GAGAGTGCAGCAGTTGGGACTCGCATTCCTCCCTGGACAGTGCA	491
m-PC	436	GAGAGTGCCTCTCTGCACACACGAATCCCCCTTGGACAGAGCTCTTGACCA	485

FIG. 5B

T416	492	AGATGTTGGGAAAATTCCCTCCACACATACTCGCTCTCTGCCAATGATT	541
m-PC	486	AGACACGGGTCCTAACAGCTTATATTCCTACTCCCTGTCTCTCCAGTGAAC	535
T416	542	TTTTTAATATCGAGGTTTCGGACCAGGACTGATGGAGCCAAGTATGCAGAA	591
m-PC	536	ACTTTGCCCTGGATGTATTGTGGCCCTGATGAGACCAACAATGCAGAG	585
T416	592	CTCATAGTGGTCAGAGAGTTAGATCGGGAGCTGAAGTCAAGCTACGAGCT	641
m-PC	586	CTTGTGGTGAAGGAGTTGGACAGGGAACCTCCACTCATATTTTGATCT	635
T416	642	TCAGCTCACTGCCCTCAGAC.ATGGGAGTACCTCAGAGGTCCTGGCTCATCC	690
m-PC	636	GGTGCTGACCGCCCTATGACAAATGGGAAT.CCCCCCTAAGTCAGGAATCAGC	684
T416	691	ATACTAAATAAGCATTTTCAGACTCCAATGACAACAGCCCTGCTTTTGA	740
m-PC	685	GTGGTCAAGGTCAATGTCTCTGGACTCCAATGACAATAAGTCCAGTGTTCGC	734

FIG. 5C

T416	741	GCAGCAATCTTATATAATAACAACCTCTTAGAAAACTCCCCGGTTGGCACTT	790
m-PC	735	TGAGAGTTCACTAGCACTAGAAAAATCCAGAGAAGACACTGTTCCCTGGTACTC	784
T416	791	TGCTCTTAGATCTGAATGCCACGGATCCAGATGAGGGCGCTAATGGGAAA	840
m-PC	785	TTCTCATAAACCTGACTGCTACAGATCCCCGACCAAGGACCCAATGGGGAG	834
T416	841	ATTGTATATTCCCTTCAGCAGTCATGTGTCTCCCCAAAAATTATGGAGACTTT	890
m-PC	835	GTAGAGTTCTTCTTTGGCAAGCATGTGTCTCCCCAGAGGTGATGAACACCTT	884
T416	891	TAAAAATTGATTCTGAAAAGAGGACATTTGACTCTTTTCAAGCAAGTGGATT	940
m-PC	885	TGGCATAGATGCCAAGACAGCGCCAGATCATCTCGGCCAAGCCCTAGATT	934
T416	941	ATGAAATCACCCAAATCCCTATGAGATTGATGTTCAGGCTCAAGATTGGGT	990
m-PC	935	ACGAGAAGAACCCTGCCTATGAGGTGGATGTCCAGGCAAGGGATTGGGT	984

FIG. 5D

T416	991	CCAAATTCAATCCCAGCCCAATTGCAAAATATAATTAAAGTTGTGGATGT	1040
m-PC	985	CCCAATTCCAATCCCAGGCCAATTGCAAAAGTTCTTATCAAAAGTTCTGGATGT	1034
T416	1041	TAATGACAATAAACCTGAAATTAAACATCAACCTCATGTCCCTTGAAAAAG	1090
m-PC	1035	CAATGACAATGCCCC.....AAGCATCCTCATCACGT....GGGCCTCC	1074
T416	1091	AAGAAATATCTTATATTTTGAAGGGGATCCTATTGATAACATTTGTTGCT	1140
m-PC	1075	CAGACGTCGCT..GGTGTCAAGAAAGATCTTCCAGGGATAGCTTCATTGCC	1122
T416	1141	TTGGTCAGAGTTCAGGACAAAGGATTCTGGGCTGAATGGAGAAATAGTTTG	1190
m-PC	1123	CTTGTCAGTGCGAATGACTTGGACTCAGGAAACAACGGTCTCGTCCACTG	1172
T416	1191	TAAGCT...TCATGGACATGGTCACCTTTAAACTTCAGAAAGACATATGAAA	1237
m-PC	1173	TTGGCTGAATCAAGAGCTGGGGCCACTTCAGACTGAAAAGGACTAACGGCA	1222

FIG. 5E

T416	1238	ACAATTATTTAATCTTAAC [·] TAAATGCCACACTGGGATAGAGAAAAGAGATCT [·]	1287
m-PC	1223	ACACGTACATGCTGCTCACC [·] CAATGCCACACTGGACACAGAGCAGTGGCCC	1272
T416	1288	GAGTATAGTTTGACTGTAA [·] TCGCTGAGGACAGGGGGACACCCAGTC [·] .TC	1335
m-PC	1273	ATATATACTCTCACTGTGT [·] TGCCCCAAGAC.CAAGGAC.CCCAGCCCTTA	1320
T416	1336	TCTACAGTGAAACATTTTACAGTTCAA [·] AATCAATGATATCAATGACAATCC	1385
m-PC	1321	TCAGCTGAGAAGGAGCTCCAA [·] ATTCAAGTTAGTGTCAATGACAATGC	1370
T416	1386	ACCCCACTTCCAGAGAAAGCCGATATGA [·] ATTGTAAATTCAGAAAAATAACT	1435
m-PC	1371	CCCTGTGTTTGAGAGAGAGCCGGTACGAGGTCTCCACTTGGGAAAAATAACC	1420
T416	1436	CACCAGGGGCATATATCACC [·] ACTGTTACAGCCACAGATCCTGATCTTGA	1485
m-PC	1421	CACCCCTCTCTTCACCTCATCAGCTCAAAGCGCATGATGCTGACTTGGGC	1470

FIG. 5F

T416	1486	GAAAATGGGCAAGTGACATACACCATCTTGA.GAGTTTATTCT.AGGA	1533
m-PC	1471	AGTAATGGAAAAGTGTATACCGTATCAAGGACTCCCCCGTTTCTCACTT	1520
T416	1534	AGTTCCATAACTACATATGTAACCATTGA...CCCATCTAATGGAGCCAT	1580
m-PC	1521	AGT..CATTATTGACTTTGAAACAGGAGAAGTCACTGCTCAGAGGTCACT	1568
T416	1581	...CTATGCCC...TCAGAAATCTTTGA..TC...ATGA.AGAAGTGAGTC	1618
m-PC	1569	GGACTATGAACACAGATGGCAGGCTTTGAGTTCAGGTGATAGCAGAG.GAC	1617
T416	1619	AGATCAC.TTTTGTGGTAGAAGCAAGAGATGGAGGAAGCCCGAAGCAACT	1667
m-PC	1618	AGAGGGCAACCCAGCTCGCATCCAG.CATCTCGGTGTGGGTAGCCTCT	1666
T416	1668	GGTAAGC.....AATACCACAGTTGTG.CTCACC.....ATCATTGAC	1704
m-PC	1667	TGGATGCCAATGATAATGCCCCAGAAAGTGATTACGCCCTGTGCTCAGTGAA	1716

FIG. 5G

T416	1705	GAAAATGACAACGTTCTGTGGTTATA.....GGGCC.....	1736
m-PC	1717	GGCAAAGCCACCCCTTTCGGTGCTTGTAATGCCTCCACGGCCACCTTCT	1766
T416	1737	..TG..CATTGCGTA.....AT.AATACGGCAGAAATCACCATTCT	1771
m-PC	1767	GTTGCCCATTGAGAATCCAGTGGCATGGATCCAGCAGGTACTGGTATAC	1816
T416	1772	..CCAAAGG.GGCTGAAAG....TGG.CTTT.CATGTCACAAGAAATAAGG	1812
m-PC	1817	CACCAAAGGCTACCCACAGCCCCCTGGTCTTTCCCTTTTGTTAACAATCGTG	1866
T416	1813	GCAATTGACAGAGACTCTGGTGTGAATGCTGAACCTCAGCTGCGCCATAGT	1862
m-PC	1867	GCTAGGGATGCAGACTCGGGGGCCCAATGGGGAACCTCTTCTACAGCATTCA	1916
T416	1863	AGCAGGTAATGAGGAGAAATATCTTCATAAATTGATCCACGATCATGTGACA	1912
m-PC	1917	AAGTGGGAATGATGCTCATCTCTT.TTTCCTCAGCC.CTTCCCTTGGGGCA	1964

FIG. 5H

T416	1913	TCCAT..ACCAACGTTAGC.ATGGATTCTGTTCCTTCCCTACACAG..AATGGG	1957
m-PC	1965	GCTATTCAATTAATGTCACCAATGCCAGCAGCCTCATCGGGAGTCAGTGGG	2014
T416	1958	AGCTGTCAAGTTATCATTCAGGACAAAGGCAATCCTCAGCTACATACCAAA	2007
m-PC	2015	ACCTGGGGATAGTGGTAGAGGACCAGGGCAGCCCTCCTTGCAGACCCAA	2064
T416	2008	GTCCCTTCTGAAGTGCATGATCTTTGAATATGCAGAGTCGGTGACAAGTAC	2057
m-PC	2065	GTTTCATTGAAGGTCGTG...TTTG..TCACCAGTGT..GGACCACCTAA	2107
T416	2058	AGCAATGACTTCAGTAAGCCAGGCATCCTTGGATGTCTCCATGA.TAATA	2106
m-PC	2108	GGGATTCTGCTCA.TGAGCCCGGAGTTCT..GAGCACACCAGCAGCTGGCT	2154
T416	2107	ATTATTTCCCTTAGGAGCAATTGTGTCAGTGTTCGCTGGTTATTATGGTGCT	2156
m-PC	2155	TTGATCTGCCCTGGCTGTACTGCTGGCCATCTTTGGATTGCTCTTAGCCCT	2204

FIG. 5I

T416	2157	ATTTGCAACTAGGTGTAACCGCGAGAAAGACACACTAGATCCTATAACT	2206
m-PC	2205	GTTCGTGTCCATCTGCAGGACAGAGAGAAAAGGATAATAGGGCCCTACAAC	2254
T416	2207	GCAGGGTGGCCGAATCAACTTACCAGCACCCACCAAAAAGGCCATCCCGG	2256
m-PC	2255	GTCGAGAAGCTGAGTCGTCAATACCGCCACCAAGCCCAAGAGGCCCCAGAAA	2304
T416	2257	CAGATTCACAAAGGGGACATCACATTGGTGCCCTACCATAAATGGCACTCT	2306
m-PC	2305	CACATTCAAGAAGGCAGATATCCACCTGGTGCCCTGTGCT.TAGGGCCAC.	2352
T416	2307	GCCCATCAGATCTCATCA...CAGATCGTCTC.CATCTTCATCTCCTA..	2350
m-PC	2353	GAGAATGAGA.CTGATGAAGTCAGGCCATCTCACAAAGGATACCAGCAAGG	2401
T416	2351	..CCTTAGAAAAGAGGGCAGATGGG.....CAGCCGGCAGAGTCACAA	2390
m-PC	2402	AGACACTGATGGAGGCAGGCTGGGACTCTTGCCCTGGAGGCCCCCTTCCAC	2451

FIG. 5J

T416	2391	CAGTCACCAGTCACTCAACAGTTTGGTGACAAATCTCATCAAACCACG...	2437
m-PC	2452	CTCACACCA.ACCCTATACAGGACCCTGCGTAACCAAGGCAACCAGGAG	2500
T416	2438	...TGCCAGA.....GAATTCT.CATTAGAAC.TCACC...CACGCC	2472
m-PC	2501	AAC TGGCAGAGAGCCAGGAGTACTGCAGGACACCTTCAACTTCTCTTT	2550
T416	2473	ACTCCTGC..TGTTGA.GCAGGTCTCTC...AGCTTCT...TTCAATGC	2512
m-PC	2551	AACCATCCAGGCAGAGAGGAATGCCTCCCGGAGAACCTAAACCTTCCTGA	2600
T416	2513	TTCAACCAGGGCAATA..TCAGCCAAGACCAAG..TTTTCGAGGAAACAA	2558
m-PC	2601	GTCCCCACCTGCTGTACGCCAACCACTCTTAAGGCCCTCTGAAGGTGCCTG	2650
T416	2559	ATATTCCAGGAGCTACAGATA.TGCCCTTCAAGACATGGACAAATTAGC	2607
m-PC	2651	GTAGCCCCATAGCGAGGGCGACTGGAGACCAAGACAAGGAGGA...GGC	2696

FIG. 5K

T416	2608	TTGAAAGACAGTGGCCGTGGTGACAGTGAGGC..AGGAGACAG.TGATT	2654
m-PC	2697	CCCACAGAGCCCCACCAGCGTCCCTCTGCAACCCTAAGACGACACAGCGGAATT	2746
T416	2655	TGATTGGGGCGAGATTCTCCAATA.GATAGGCTGCTGGGTGAAGGATTC	2703
m-PC	2747	TCAAT..GGCAAAGTGTCTCCTAGAGGAGAGTCCGGTCCCTCATCAGATTC	2794
T416	2704	..AGCGACCTGTTT...CTCACAGATGGAAGAATTCCAGCAGCTATGAGA	2748
m-PC	2795	TGAGGAGCCCTGGTTAGGCTCTCTG.TGGCTGCTTTTGCGGA...ACGGAA	2840
T416	2749	CTCTGCACGGAGGAG..TGCAGGGTCCTGGGACACTCTGACCAGTGCTGG	2796
m-PC	2841	CCCGG..TGGAGGAGCCTGCTGGGACT..CTCCTCCTGTCCAGCAAATC	2886
T416	2797	ATGCCACCACCTGCCCTCAC...CGTCTTCTGATTATAGGAGTAACATGT	2842
m-PC	2887	TCCCAGCTGCTGCTCCTTGCTGCACCCAGGGCCAATTCCAGCCCAACCAAA	2936

FIG. 5L

T416	2843	TCATTCCAGGGGAAGAAATTCCCAACGCAACCCAGCAGCAGCATC.....	2887
m-PC	2937	CCA..CCGAGGAAATAAATACTTGGCCAAGCCCCGGCGCAGCAGCAGGGG	2984
T416	2888	.CACATCAGAGTC.TTGAGGATGACGCTCAGCCTGCAGATTCCGGTGAAA	2935
m-PC	2985	TACCATCCCAGACACAGAGGGCCTTG.TAGGCCCTCAAGCCT.AGTGGCCA	3032
T416	2936	AGAAGAAGAGTTTTTCCACCTTTTGGAAGGACTCCCCAAACGATGAGGAC	2985
m-PC	3033	AGCAGAA.....CCTGACCCTGGAAGAAGGGC.CCCCGAGCCCGGAGGA.	3074
T416	2986	ACTGGGGATACCAGCACATC.ATCTCTGCTCTCGGAAATGAGCAGTGTGT	3034
m-PC	3075	...GGACCTTTCTGTAAAGCGACTTCTAGAAGAAGAGCTGTCGAGCCTGT	3121
T416	3035	TCCAGCGTCTCTTACCGCCTTCCCTGGACA..CCTATTCTGAATGCAGTG	3082
m-PC	3122	TGGACCCCTAATACAGGTCTAGCCCTGGACAAGCTGAGTCCGCCTGACCCA	3171

FIG. 5M

T416	3083	AGGTGGATCG.GTCCAACTCCCTGGAGCGCAGGAAGGAGCCCTTGCCAGC	3131
m-PC	3172	GCCTGGATGGCGAGATTGTCAATTGCCCCCTCA.....CCACCAATTATCGA	3216
T416	3132	CAAAACTGTGGGTTACCCACAGGGGGTAGCGGCATGGGCAGCCAGTACGC	3181
m-PC	3217	GACAACT.TGTCTTCCCCCGATGCTACAACATCAGAGGAACCGAGAAC..	3263
T416	3182	ATTTTCAAAATCCCAACCACTGTGGGCCGCCACTTGGAACCTCACTCC	3231
m-PC	3264	.CTTCCAGACATTCCGGCAAGACAGTTGGACCCGGGAC.CCGAGCTGAGCCC	3311
T416	3232	AGTGTGCAGCCTTCTTCAAAATGGCTGCCAGCCATGGAGGAGATCCCT..	3279
m-PC	3312	AACAGGCACGCGCCTGGCCAGCACTTTCGTCTCGGAGATGAGCTCTCTGC	3361
T416	3280	..GAAA..ATTATGAGGAAGATGATTTTGACAATG..TGCT.CAACCACC	3322
m-PC	3362	TGGAATGTGTGTGGGCAGCACACGGTACCAGTGGAAGCTGCGTCCGCG	3411

FIG. 5N

T416	3323	TCAATGATGGGAAACACGAACTCATGGATG.....CCAGT...GA.....	3359
m-PC	3412	GCTTTGCGGAGGCTCTCGGTGTGCGGGAGGACCCCTCAGTCTAGACCTAGC	3461
T416	3360ACTGGTGGCAGAGATTAAACA..ACTGCTT..CAAGATGTCCGC.C	3400
m-PC	3462	CACCAAGTGGGGCTTCAGCTTCAGAAAGCACAGGGTAGAAAGAAGGCAGCTG	3511
T416	3401	AGAGC.....	3405
m-PC	3512	AGAGCAGACTTGGCTGTGGCAGGAATCTA	3540

FIG. 50

m-PC	1	MMLLLPFLGLLPGSYLFI	SGDCQEVATVMVKFQVTEEVPSGT	VIGKLS	50			
T416	1	MHQMNAKMHFRFV	FALLIVSFN.HDVLGKNLKYRIYEEQR	VGSVIARLS	48			
m-PC	51	QELR..VEERRGKAGDA	FQILQLPQALPVQMNSE	DGLLSTSSRLDREKLC	98			
T416	49	EDVADVLLKLPNPST	VRFRAMQRGNSPLL	VVNEDNGEISIGATIDREQLC	98			
m-PC	99	RQEDPCLVSFDV..LATGASALIH	VEIQVLDINDHQPF	PKDEQELEISE	146			
T416	99	QKNLNC	SIEFDVITLPT	TEHLQLFHIEVEVLDINDNSPQFSRSLPIEISE	148			
m-PC	147	SASLHTRIP	LDRA	LDQDTGPN	SLYSLS	SPSEHFALDVIVGPD	ETKHAEL	196
T416	149	SAAVGTRIP	LD	SAFDPDV	GENSLHTY	SLSANDFFNIEV	TRTRTDGAKYAE	198
m-PC	197	VVVKELDRE	LHSYFDL	VLTA	YDNGNPPKSGIS	VVKVNVLD	SDNSNDNSPVFAE	246
T416	199	IVVRELDRE	LKSSYELQ	LTA	SDMGVPQR	SGSSILKISIS	SDSDNSNDNSPAFEQ	248

FIG. 6A

m-PC	247	SSLALEIPEDTVPGTLLINLTATDPDQGPNGEVEFFFGKHVSPVMTTFG	296
		: : : . . : : :	
T416	249	QSYIIQLLENSPVGTLTLLDLNATDPDEGANGKIVYSFSSHVSPKIMETFK	298
m-PC	297	IDAKTGQIILRQALDYEKNPAYEVDVQARDLGPNSIPGHCKVLIKVLDVN	346
		. . : . . . : :	
T416	299	IDSERGHLTLFKQVDYEITKSYEIDVQAQDLGPNSIPAHCKIIIKVVDVN	348
m-PC	347	DNAPSILITWAS...QTSLVSEDLPRDSFIALVSANDLDSGNNGLVHCW	392
		: : : : : : : : : :	
T416	349	DNKPEININLMSPGKEEISYIFEGDPIDTFVALVRVQDKDSGLNGEIVCK	398
m-PC	393	LNQELGHFRLKRTNGNTYMLLTNATLDREQWPIYTLTVFAQDQGPQLSA	442
		. : : . . : :	
T416	399	LHGH.GHFKLQKTYENNYLILTNAATLDREKRSEYSLTVIAEDRGTPSLST	447
m-PC	443	EKELQIQVSDVNDNAPVFEEKSRYEVSSTWENNPPSLHLITLKAHDADLGSN	492
		: : : : : : : : : .	
T416	448	VKHFTVQINDINDNPPHFQRSRYEFVISENNSPGAYITTVTATDPDLGEN	497

FIG. 6B

m-PC	493	GKVSRIKD.....SPVSHLVIIDFETGETAQRSLDYEQMAGFEFQVIA	537
	:::	
T416	498	GQVTTYILESFILGSSITTYVTIDPSNGAIYALRIFDHEEVSQITFVVEA	547
m-PC	538	EDRGQP.QLASSISVWVSLLDANDNAPEVIQPVLSEGKATLSVLVNASTG	586
	::	
T416	548	RDGGSPKQLVSNTTVVLTIIDENDNVVVGIPALRNNTAEITIPKGAESG	597
m-PC	587	HLLPIENPSGMDPAGTGIPPKATHSPWSFLLLTIVARDADSGANGELFY	636
	:	
T416	598FHVTRIRAI DRDSGVNAELSC	618
m-PC	637	SIQSGNDAHLFFLSPSLGQLFINVTNASSLIGSQWDLGIVVEDQGSPSLQ	686
	: . .: . .: . .: . .: . .: . .	
T416	619	AIVAGNEENIFIIDPRSCDIHTNV.SMDSVPYTEWELSVIIQDKGNPQLH	667
m-PC	687	TQVSLKVV...FVTSVDHLRDSAHEPGVLSTPALALICLAVLLAIFGLLL	733
	: . .: . .: . .: . .: . .: . .	
T416	668	TKVLLKCMIFEYAESVTSTAMTSVVSQASLDVSMIIISLGAICAVLLVIM	717

FIG. 6C

m-PC	734	ALFVSI	CRTER	KNRAY	NCREAE	SSYRHQ	PKRPQ	KHIQ	KADI	HLVP	VLRA	783
		.									:	
T416	718	VL	FATRC	NREK	KDTRS	YNCR	VAESTY	QHHP	KRPS	RQIH	KGDITL	767
m-PC	784	HENET	DEV	..PSH	KDTS	KETL	MEAG	WDSC	LEAP	FHLT	PTLY	831
											:	
T416	768	TL	FIRSH	RSSP	SSPT	LERG	QMGS	RQSH	NSHQ	SLNS	LVTI	817
m-PC	832	Q	GELAE	SQEV	LQDT	TFN	FLFN	HPRQ	RNAS	REN	LNLP	881
		.										
T416	818	S	LELTH	ATPA	VEQV	SQLL	SMLH	QGQY	QPRP	SFRG	NKYSR	867
m-PC	882	V	P	G	S	P	I	A	R	A	T	931
		:	:	:	:	:	:	:	:	:	:	
T416	868	F	S...	L	K	D	S	G	R	G	D	913
m-PC	932	L	R	S	L	V	R	L	S	V	A	981
			
T416	914	A	M	R	L	C	T	E	E	C	R	963

FIG. 6D

m-PC	982	GNKYLAKPGGSSRG	TIPDTEGLVGL.KPSGQAE	PDLEE	GPPSPEED	LSVK	1030
T416	964	HQSEDDAQPADS	GEKKSFSTFGK	DSPNDEDTG	DTSTSSLLSEM	SSVFQ	1013
m-PC	1031	RLLEEEL...	SSLDPNTGLALDKL	SPDPAMMARLS	PLTTNYRDN	LS	1077
T416	1014	RLPPSLD	TYSECSEVDRS	NSLERRKGPL	PAKTVGYPQ	GVAAWAASTHFQ	1063
m-PC	1078	PDAT	TSEEPRTFQTFG	KTVGPGPELS	PTGTRLASTFV	SEMSSLLEMLLGQ	1127
T416	1064	NPTNCGPPLG	THS...SVQPSS	KWLPAMEE	IPENYEED	DDFDNVLNHLND	1110
m-PC	1128	HTVPVEA	AASAAALRR	LSVCGRTL	SLDLATSGASA	SEAQQGRKKAES	RLGCCGRNL 1180
T416	1111	GKHE	MDASELVAE	INKLLQD	VRQS.....		1135

FIG. 6E

GAAGTGGGAT	GTGCAAAAGC	GCCGGCTGGA	AATCCCGGCT	GTGTCTCCGT	CAACTCTTTA	60
CGCAACAGAG	GTCTCCCCCT	GCCCTTGTT	TCTACCGGC	CGCCTGCTCC	CACTCGGCGA	120
AAAAAATTAC	ACAACAGCAG	CCGCGGCG	ATG ACG TGG	AGG GCT GCC	TCC	172
	Met Thr Trp Arg	Ala Ala	Ala Ser			8
ACG TGC GCG	GCG CTC	CTG ATT	CTG CTG TGG	GCG CTG ACG	ACC GAA GGT	220
Thr Cys Ala	Ala Leu	Ile Leu	Leu Trp	Ala Leu Thr	Thr Glu Gly	24
GAT CTG AAA	GTA GAG	ATG ATG	GCA GGG	GGG ACT CAG	ATC ACA CCC CTG	268
Asp Leu Lys	Val Glu Met	Met Ala	Gly Thr	Gln Ile Thr	Pro Leu	40
AAT GAC AAT	GTC ACC	ATA TTC	TGC AAT	ATC TTT TAT	TCC CAA CCC CTC	316
Asn Asp Asn	Val Thr	Ile Phe	Cys Asn	Ile Phe Tyr	Ser Gln Pro Leu	56
AAC ATC ACG	TCT ATG	GGT ATC	ACC TGG	TTT TGG	AAG AGT CTG ACG TTT	364
Asn Ile Thr	Ser Met Gly	Ile Thr	Trp Phe	Trp Lys Ser	Leu Thr Phe	72
GAC AAA GAA	GTC AAA	GTC TTT	GAA TTT	GGA GAT	CAC CAA GAG GCA	412
Asp Lys Glu	Val Lys Val	Phe Glu	Phe Phe	Gly Asp His	Gln Glu Ala	88
TTC CGA CCT	GGA GCC	ATT GTG	TCT CCA	TGG AGG	CTG AAG AGT GGG GAC	460
Phe Arg Pro	Gly Ala	Ile Val	Ser Pro	Trp Arg	Leu Lys Ser Gly Asp	104
GCC TCA CTG	CGG CTG	CCT GGA	ATC CAG	CTG GAG	GAA GCA GGA GAG TAC	508
Ala Ser Leu	Arg Leu	Pro Gly	Ile Gln	Leu Glu	Ala Gly Glu Tyr	120

Fig. 7A

CGA TGT GAG GTG GTG GTC ACC CCT CTG AAG GCA CAG GGA ACA GTC CAG	556
Arg Cys Glu Val Val Val Thr Pro Leu Lys Ala Gln Gly Thr Val Gln	136
CTT GAA GTT GTG GCT TCC CCA GCC AGC AGA TTG TTG CTG GAT CAA GTG	604
Leu Glu Val Val Ala Ser Pro Ala Ser Arg Leu Leu Asp Gln Val	152
GGC ATG AAA GAG AAT GAA GAC AAA TAT ATG TGT GAG TCA AGT GGG TTC	652
Gly Met Lys Glu Asn Glu Asp Lys Tyr Met Cys Glu Ser Ser Gly Phe	168
TAC CCA GAG GCT ATT AAT ATA ACA TGG GAG AAG CAG ACC CAG AAG TTT	700
Tyr Pro Glu Ala Ile Asn Ile Thr Trp Glu Lys Gln Thr Gln Lys Phe	184
CCC CAT CCC ATA GAG ATT TCT GAG GAT GTC ATC ACT GGT CCC ACC ATC	748
Pro His Pro Ile Glu Ile Ser Glu Asp Val Ile Thr Gly Pro Thr Ile	200
AAG AAT ATG GAT GGC ACA TTT AAT GTC ACT AGC TGC TTG AAG CTG AAC	796
Lys Asn Met Asp Gly Thr Phe Asn Val Thr Ser Cys Leu Lys Leu Asn	216
TCC TCT CAG GAA GAC CCT GGG ACT GTC TAC CAG TGT GTG GTA CGG CAT	844
Ser Ser Gln Glu Asp Pro Gly Thr Val Tyr Gln Cys Val Val Arg His	232
GCG TCC TTG CAT ACC CCC TTG AGG AGC AAC TTT ACC CTG ACT GCT GCT	892
Ala Ser Leu His Thr Pro Leu Arg Ser Asn Phe Thr Leu Thr Ala Ala	248
CGG CAC AGT CTT TCT GAA ACT GAG AAG ACA GAT AAT TTT TCC ATT CAT	940
Arg His Ser Leu Ser Glu Thr Glu Lys Thr Asp Asn Phe Ser Ile His	264

Fig. 7B

TGG TGG CCT ATT TCA TTC ATT GGT GTT GGA CTG GTT TTA TTA ATT GTT	988
Trp Trp Pro Ile Ser Phe Ile Gly Val Gly Leu Val Leu Ile Val	280
TTG ATT CCT TGG AAA AAG GTA AGG GGC TCC AAA GCA AAG TTC AGC CCT	1036
Leu Ile Pro Trp Lys Lys Val Arg Gly Ser Lys Ala Lys Phe Ser Pro	296
GTG TCT TGG GCT AGT AAA AAG CTT TTA GAG CAG CTG CTG CCA ACC TTA	1084
Val Ser Trp Ala Ser Lys Lys Leu Leu Glu Gln Leu Pro Thr Leu	312
CAA GCC TCA AGG GAC AGG CCT GCT GGA AAG GAC TTT GTC AGT CCC TCT	1132
Gln Ala Ser Arg Asp Arg Pro Ala Gly Lys Asp Phe Val Ser Pro Ser	328
TCA CCA TCA GGT GTT GGG AAT GTT GGC TGT CCA ATC CAG TTT CCT	1180
Ser Pro Ser Gly Val Gly Asn Val Gly Cys Val Pro Ile Gln Phe Pro	344
ATC ACA GAG GAC CTA GCT GTC ACA TAC CAT CTG ACC TCT GTA TGG TGG	1228
Ile Thr Glu Asp Leu Ala Val Thr Tyr His Leu Thr Ser Val Trp Trp	360
TTT GTG ACT CTG GGG TGATGTGTTG TAAAGCCTCC CTCTCTTTCT CCATACTAAA	1283
Phe Val Thr Leu Gly	365
CAAGTATTAT ATCTCTGTGA ATGAACCAGA CTTTAGTGTT CAGACCAGGC CCTGAACTAT	1343
GTGTGGACTG CTTGTTTTTC TCACACATTT AGAAACTATG GCTTAGAGAG GGAATTCCT	1403
CATATTTTAT CTGATCAATA ACTGACCACC AGATCTCACT AGTTTGACTA AGAATTTCTA	1463
ACCCTCACTA GGTATTTCTA AACTAAAACA TGTTTCTAAA CATTTTATC CCTGACTATG	1523

Fig. 7C

GCCCAAATAG	TAAATAAAAC	AGCTCAAGCT	TTAGAGGCC	AAGAGACCTA	TGTAAATGTG	1583
TTGGTTAAAA	TAGTTTTAGA	TAATAAAAGG	GCCCTCAATT	ATTTATGGGC	CTGTCAAGGC	1643
AAAATCTGCA	CAACAGCCAG	TACATCTCAT	TATAAATAAT	TTAGGAGAAG	TGGAATAATC	1703
AGTCAATTAA	GAAAAATGGC	CCTTTATCTA	AAGTTGGCCA	TTTAGATTCA	CGGACTTAT	1763
TCCCTGTTGA	TCTAGGCCAT	GAGAAAACTG	GATAAAAAGT	GTTTTCAAA	TGTTTCTTGT	1823
GGTATTTGTG	ACTGTTGTCA	TATTTCTTGC	CTTTCCTCTG	TTC'TGATATT	CAGGTGCTAT	1883
TGAGAGAGGA	GGAAGGAAGA	AACTAGTCAG	GCAGGCAGTT	AGGTTGGCC	CTCAGTCAAA	1943
TTTCCTTCAA	CAAAAGAAC	GCCTGAAAAA	TCAAACCTGCA	GATAAGGAA	CTTGTACAGG	2003
GGGGCTTGCC	TAAAACATGC	CCACAGCCAC	ATACATTAAA	ACAAGGCTAC	ACAGGAGACT	2063
TGCCCTAGACA	TGCTCACAAAT	AGAAAATTCC	ATCCCCCTGAC	ACATGCACAG	TAAGGGGAAC	2123
AAAGCCACAT	GGAGTAACTC	AAGCTAAGGG	CTTGCAATGCA	CAC'TACGAGG	ATGGGGTGGA	2183
GCTACCAGAA	ATGTGTGCCCT	TATGCCTTTGT	TATTCAGCTG	TGAAAATGGCA	ACCCTCTTTT	2243
GGGCCCCCTC	TCTGCAGTGG	AGTGCTTTCT	TCTTTTGTCTT	ATTAAACTTT	CACTTCAACT	2303
TCAAAAAAA	AAAAAAA	AAAAAAA				2330

Fig. 7D

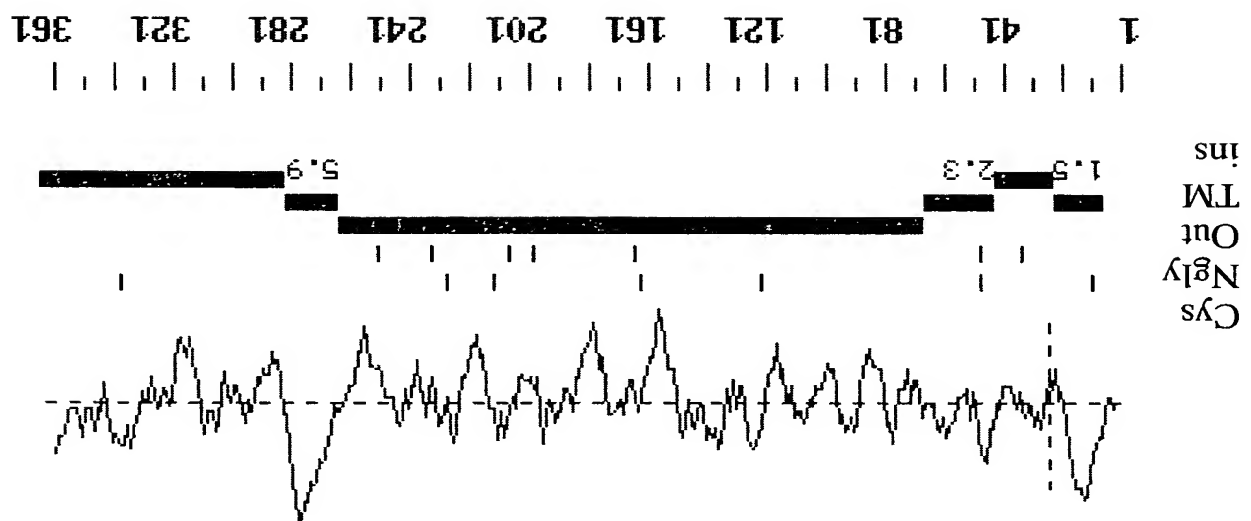


Fig. 8

GAAGTTGAAG	TGAAAGTTTA	ATAAGCAAAA	GAAGAAAGCA	CTCCACTGCA	GAGAGGGGGC	2246
GAAGTTGAAG	TGAAAGTTTA	ATAAGCAAAA	GAAGAAAGCA	CTCCACTGCA	GAGAGGGGGC	121136
CCAAAAGAGG	GTGCGCATTT	CACAGCTGAA	TACAAAAGGCA	TAAGGCACAC	ATTTCTGGTA	2186
CCAAAAGAGG	GTGCGCATTT	CACAGCTGAA	TACAAAAGGCA	TAAGGCACAC	ATTTCTGGTA	121196
GCTCCACCCC	ATCCTCGTAG	TGTGCATGCA	AGCCCTTAGC	TTGAGTTACT	CCATGTGGCT	2126
GCTCCACCCC	ATCCTCGTAG	TGTGCATGCA	AGCCCTTAGC	TTGAGTTACT	CCATGTGGCT	121256
TTGTTCCCCCT	TACTGTGCAT	GTGTCAGGGG	ATGGAATTTT	CTATTGTGAG	CATGTCCTAGG	2066
TTGTTCCCCCT	TACTGTGCAT	GTGTCAGGGG	ATGGAATTTT	CTATTGTGAG	CATGTCCTAGG	121316
CAAGTCTCCT	GTGTAGCCTT	GTTTTAATGT	ATGTGGCTGT	GGCATGTTT	TAGGCAAGCC	2006
CAAGTCTCCT	GTGTAGCCTT	GTTTTAATGT	ATGTGGCTGT	GGCATGTTT	TAGGCAAGCC	121376
CCCCGTGTACA	AGTTCCCCTTA	TCTGCAGTTT	GATTTTTCAG	GCTGTTCTTT	TGTTTGAAGG	1946
CCCCGTGTACA	AGTTCCCCTTA	TCTGCAGTTT	GATTTTTCAG	GCTGTTCTTT	TGTTTGAAGG	121436

Fig. 9A

AATTGACTG	AGGGCCACC	CTAACTGCCT	GCCTGACTAG	TTTCTTCCCTT	CCTCCTCTCT	1886
AATTGACTG	AGGGCCACC	CTAACTGCCT	GCCTGACTAG	TTTCTTCCCTT	CCTCCTCTCT	121496
CAATAGCACC	TGAATATCAG	AACCAGAGAA	AGCAAGAAA	TATGACAACA	GTCACAAATA	1826
CAATAGCACC	TGAATATCAG	AACCAGAGAA	AGCAAGAAA	TATGACAACA	GTCACAAATA	121556
CCACAAGAAA	CATTGAAA	CCACTTTT	TCCAGTTTC	TCATGGCCTA	GATCCAACAG	1766
CCACAAGAAA	CATTGAAA	CCACTTTT	TCCAGTTTC	TCATGGCCTA	GATCCAACAG	121616
GAATAAGTCC	CGTGAATCTA	AATGGCCAAC	TTTAGATAAA	GGGCCATTTT	TCTTAATTGA	1706
GAATAAGTCC	CGTGAATCTA	AATGGCCAAC	TTTAGATAAA	GGGCCATTTT	TCTTAATTGA	121676
CTGATTATTC	CACCTCTCCT	AAATTATT	TAATGAGATG	TACTGGCTGT	TGTGCAGATT	1646
CTGATTATTC	CACCTCTCCT	AAATTATT	TAATGAGATG	TACTGGCTGT	TGTGCAGATT	121736
TTGCCTTGAC	AGGCCATAA	ATAATTGAGG	GCCCTTTTAT	TATCTAAAAC	TATTTTAACC	1586
TTGCCTTGAC	AGGCCATAA	ATAATTGAGG	GCCCTTTTAT	TATCTAAAAC	TATTTTAACC	121796

Fig. 9B

AACACATTTA	CATAGGTCTC	TTGGGCCCTCT	AAAGCTTGAG	CTGTTTATT	TACTATTGG	1526
AACACATTTA	CATAGGTCTC	TTGGGCCCTCT	AAAGCTTGAG	CTGTTTATT	TACTATTGG	121856
GCCATAGTCA	GGGATAAAA	TGTTTAGAAA	CATGTTTAG	TTTAGAAAATA	CCTAGTGAGG	1466
GCCATAGTCA	GGGATAAAA	TGTTTAGAAA	CATGTTTAG	TTTAGAAAATA	CCTAGTGAGG	121916
GTTAGAAAATT	CTTAGTCAA	CTAGTGAGAT	CTGGTGGTCA	GTTATTGATC	AGATAAAAATA	1406
GTTAGAAAATT	CTTAGTCAA	CTAGTGAGAT	CTGGTGGTCA	GTTATTGATC	AGATAAAAATA	121976
TGAGGAATTC	CCCTCTCTAA	GCCATAGTTT	CTAAATGTGT	GAGAAAAACA	AGCAGTCCAC	1346
TGAGGAATTC	CCCTCTCTAA	GCCATAGTTT	CTAAATGTGT	GAGAAAAACA	AGCAGTCCAC	122036
ACATAGTTCA	GGGCCTGGTC	TGAACACTAA	AGTCTGGTTC	ATTCACAGAG	ATATAATACT	1286
ACATAGTTCA	GGGCCTGGTC	TGAACACTAA	AGTCTGGTTC	ATTCACAGAG	ATATAATACT	122096
TGTTTAGTAT	GGAGAAAGAG	AGGAGGCTT	TACAACACAT	CACCCAGAG	TCACAAACCA	1226
TGTTTAGTAT	GGAGAAAGAG	AGGAGGCTT	TACAACACAT	CACCCAGAG	TCACAAACCA	122156

Fig. 9C

CCATACAGAG	GTCAGATGGT	ATGTGACAGC	TAGGTCCTCT	GTGATAGGAA	ACTGGATTGG	1166
CCATACAGAG	GTCAGATGGT	ATGTGACAGC	TAGGTCCTCT	GTGATAGGAA	ACTGGATTGG	122216
AACACAGCCA	ACATTCCCAA	CACCTGATGG	TGAAGAGGGA	CTGACAAAAGT	CCTTTCAGC	1106
AACACAGCCA	ACATTCCCAA	CACCTGATGG	TGAAGAGGGA	CTGACAAAAGT	CCTTTCAGC	122276
AGGCCTGTCC	CTTGAGGCTT	GTAAGGTTGG	CAGCAGCTGC	TCTAAAAGCT	TTTTACTAGC	1046
AGGCCTGTCC	CTTGAGGCTT	GTAAGGTTGG	CAGCAGCTGC	TCTAAAAGCT	TTTTACTAGC	122336
CCAAGACACA	GGGCTGAACT	TTGCTTTTGA	GCCCCTTACC	TTTTTCCAAG	GAATCAAAAC	986
CCAAGACACA	GGGCTGAACT	TTGCTTTTGA	GCCCCTTACC	TTTTTCCAAG	GAATCAAAAC	122396
AATTAATAAA	ACCAGTCCAA	CACCAATGAA	TGAAATAGGC	CACCAATGAA	TGAAAAAATT	926
AATTAATAAA	ACCAGTCCAA	CACCAATGAA	TGAAATAGGC	CACCAATGAA	TGAAAAAATT	122456
ATCTGTCTTC	TCAGTTTCAG	AA				904
ATCTGTCTTC	TCAGTTTCAG	CA				122478

Fig. 9D

	M	V	2
GGCCCGGCAGCTGCGGCTCGGGATCCGTCGAGGGAGGCCGAGCTTGCCAAAGCTGGCGCCAGCGGGGTC	ATG	GTG	77
P G A R G G G A L A R A A G R G L L A L			22
CCC GGC GCC CGC GGC GGC GCA CTG GCG GCT GCG GGT GGC CGG GGC CTC CTG GCT TTG			137
L L A V S A P L R L Q A E L G D G C G			42
CTG CTC GCG GTC TCC GCC CCG CTC CCG CTG CAG GCG GAG GAG CTG GGT GAT GGC TGT GGA			197
H L V T Y Q D S G T M T S K N Y P G T Y			62
CAC CTA GTG ACT TAT CAG GAT AGT GGC ACA ATG ACA TCT AAG AAT TAT CCC GGG ACC TAC			257
P N H T V C E K T I T V P K G K R L I L			82
CCC AAT CAC ACT GTT TGC GAA AAG ACA ATT ACA GTA CCA AAG GGG AAA AGA CTG ATT CTG			317
R L G D L D I E S Q T C A S D Y L L F T			102
AGG TTG GGA GAT TTG GAT ATC GAA TCC CAG ACC TGT GCT TCT GAC TAT CTT CTC TTC ACC			377
S S S D Q Y G P Y C G S M T V P K E L L			122
AGC TCT TCA GAT CAA TAT GGT CCA TAC TGT GGA AGT ATG ACT GTT CCC AAA GAA CTC TTG			437
L N T S E V T V R F E S G S H I S G R G			142
TTG AAC ACA AGT GAA GTA ACC GTC CGC TTT GAG AGT GGA TCC CAC ATT TCT GGC CGG GGT			497

Fig. 10A

F	L	L	L	T	Y	A	S	S	D	H	P	D	L	I	T	C	L	E	R	A	162
TTT	TTG	CTG	ACC	TAT	GCG	AGC	AGC	GAC	GAT	CCA	GAT	TTA	ATA	ACA	TGT	TTG	GAA	CGA	GCT	557	
S	H	Y	L	K	T	E	Y	S	K	F	C	P	A	G	C	R	D	V	A	182	
AGC	CAT	TAT	TTG	AAG	ACA	GAA	TAC	AGC	AAA	TTC	TGC	CCA	GCT	GGT	TGT	AGA	GAC	GTA	GCA	617	
G	D	I	S	G	N	M	V	D	G	Y	R	D	T	S	L	L	C	K	A	202	
GGA	GAC	ATT	TCT	GGG	AAT	ATG	GTA	GAT	GGA	TAT	AGA	GAT	ACC	TCT	TTA	TTG	TGC	AAA	GCT	677	
A	I	H	A	G	I	I	A	D	E	L	G	G	Q	I	S	V	L	Q	R	222	
GCC	ATC	CAT	GCA	GGA	ATA	ATT	GCT	GAT	GAA	CTA	GGT	GGC	CAG	ATC	AGT	GTG	CTT	CAG	CGC	737	
K	G	I	S	R	Y	E	G	I	L	A	N	G	V	L	S	R	D	G	S	242	
AAA	GGG	ATC	AGT	CGA	TAT	GAA	GGG	ATT	CTG	GCC	AAT	GGT	GTT	CTT	TCG	AGG	GAT	GGT	TCC	797	
L	S	D	K	R	F	L	F	T	S	N	G	C	S	R	S	L	S	F	E	262	
CTG	TCA	GAC	AAG	CGA	TTT	CTG	TTT	ACC	TCC	AAT	GGT	TGC	AGC	AGA	TCC	TTG	AGT	TTT	GAA	857	
P	D	G	Q	I	R	A	S	S	S	W	Q	S	V	N	E	S	G	D	Q	282	
CCT	GAC	GGG	CAA	ATC	AGA	GCT	TCT	TCC	TCA	TGG	CAG	TCG	GTC	AAT	GAG	AGT	GGA	GAC	CAA	917	
V	H	W	S	P	G	Q	A	R	L	Q	D	Q	G	P	S	W	A	S	G	302	
GTT	CAC	TGG	TCT	CCT	GGC	CAA	GCC	CGA	CTT	CAG	GAC	CAA	GGC	CCA	TCA	TGG	GCT	TCG	GGC	977	

Fig. 10B

D S S N N H K P R E W L E I D L G E K K	322
GAC AGT AGC AAC AAC CAC AAA CCA CGA GAG TGG CTG GAG ATC GAT TTG GGG GAG AAA AAG	1037
K I T G I R T T G S T Q S N F N F Y V K	342
AAA ATA ACA GGA ATT AGG ACC ACA GGA TCT ACA CAG TCG AAC TTC AAC TTT TAT GTT AAG	1097
S F V M N N F K N N S K W K T Y K G I V	362
AGT TTT GTG ATG AAC TTC AAA AAC AAT AAT TCT AAG TGG AAG ACC TAT AAA GGA ATT GTG	1157
N N E E K V F Q G N S N F R D P V Q N N	382
AAT AAT GAA GAA AAG GTG TTT CAG GGT AAC TCT AAC TTT CGG GAC CCA GTG CAA AAC AAT	1217
F I P P I V A R Y V R V V P Q T W H Q R	402
TTC ATC CCT CCC ATC GTG GCC AGA TAT GTG CGG GTT GTC CCC CAG ACA TGG CAC CAG AGG	1277
I A L K V E L I G C Q I T Q G N D S L V	422
ATA GCC TTG AAG GTG GAG CTC ATT GGT TGC CAG ATT ACA CAA GGT AAT GAT TCA TTG GTG	1337
W R K T S Q S T S V S T K K E D E T I T	442
TGG CGC AAG ACA AGT CAA AGC ACC AGT GTT TCA ACT AAG AAA GAA GAT GAG ACA ATC ACA	1397
R P I P S E E T S T G I N I T T V A I P	462
AGG CCC ATC CCC TCG GAA GAA ACA TCC ACA GGA ATA AAC ATT ACA ACG GTG GCT ATT CCA	1457

Fig. 10C

L	V	L	L	V	V	L	V	F	A	G	M	G	I	F	A	A	F	R	K	482
TTG	GTG	CTC	CTT	GTT	GTC	CTG	GTG	TTT	GCT	GGA	ATG	GGG	ATC	TTT	GCA	GCC	TTT	AGA	AAG	1517
K	K	K	K	G	S	P	Y	G	S	A	E	A	Q	K	T	D	C	W	K	502
AAG	AAG	AAG	AAA	GGA	AGT	CCG	TAT	GGA	TCA	GCA	GAG	GCT	CAG	AAA	ACA	GAC	TGT	TGG	AAG	1577
Q	I	K	Y	P	F	A	R	H	Q	S	A	E	F	T	I	S	Y	D	N	522
CAG	ATT	AAA	TAT	CCC	TTT	GCC	AGA	CAT	CAG	TCA	GCT	GAG	TTT	ACC	ATC	AGC	TAT	GAT	AAT	1637
E	K	E	M	T	Q	K	L	D	L	I	T	S	D	M	A	D	Y	Q	Q	542
GAG	AAG	GAG	ATG	ACA	CAA	AAG	TTA	GAT	CTC	ATC	ACA	AGT	GAT	ATG	GCA	GAT	TAC	CAG	CAG	1697
P	L	M	I	G	T	G	T	V	T	R	K	G	S	T	F	R	P	M	D	562
CCC	CTC	ATG	ATT	GGC	ACC	GGG	ACA	GTC	ACG	AGG	AAG	GGC	TCC	ACC	TTC	CGG	CCC	ATG	GAC	1757
T	D	A	E	E	A	G	V	S	T	D	A	G	G	H	Y	D	C	P	Q	582
ACG	GAT	GCC	GAG	GAG	GCA	GGG	GTG	AGC	ACC	GAT	GCC	GGC	GGC	CAC	TAT	GAC	TGC	CCG	CAG	1817
R	A	G	R	H	E	Y	A	L	P	L	A	P	P	E	P	E	Y	A	T	602
CGG	GCC	GGC	CGC	CAC	GAG	TAC	GCG	CTG	CCC	CTG	GCG	CCC	CCG	GAG	CCC	GAG	TAC	GCC	ACG	1877
P	I	V	E	R	H	V	L	R	A	H	T	F	S	A	Q	S	G	Y	R	622
CCC	ATC	GTG	GAG	CGG	CAC	GTG	CTG	CGC	GCC	CAC	ACG	TTC	TCT	GCG	CAG	AGC	GGC	TAC	CGC	1937

Fig. 10D

V P G P Q P G H K H S L S S G G F S P V 642
GTC CCA GGG CCC CAG CCC GGC CAC AAA CAC TCC CTC TCC TCG GGC TTC TCC CCC GTA 1997

A G V G A Q D G D Y Q R P H S A Q P A D 662
GCG GGT GTG GGC GCC CAG GAC GGA GAC TAT CAA AGG CCA CAC AGC GCA CAG CCT GCG GAC 2057

R G Y D R P K A V S A L A T E S G H P D 682
AGG GGC TAC GAC CGG CCC AAA GCT GTC AGC GCC CTC GCC ACC GAA AGC GGA CAC CCT GAC 2117

S Q K P P T H P G T S D S Y S A P R D C 702
TCT CAG AAG CCC CCA ACG CAT CCC GGG ACG AGT GAC AGC TAT TCT GCC CCC AGA GAC TGC 2177

L T P L N Q T A M T A L L * 715
CTC ACA CCC CTC AAC CAG ACG GCC ATG ACT GCC CTT TTG TGA 2219

ACACAATGTGAAGAAGCCCTGCTGGTACTGAGCGTCGGGCTGTCACAAGGCACCTGGAAGAAGGAGCCTGCTGGTCC 2298
AGAGTGTGCGGTGTATCGGTGTGTGTGTACACTTGCATGTGTGTGTGTGATCCAGTAGGATCCTAGAGACAAACCTGTC 2377
ATACTGTTTACAAAAATTGTGCAGCTGGTTTCGTGCTGACCCCTTAGGGTGGTCTGTGTTGGGTTTTTGGCTAGAAAAA 2456
TGAAAAATTTTAGATGGCGTTTTCATTCCTCTGACTGATATTGAGCTGCTTTGGTGTTAAAGGTGTAATGTGTACAGAG 2535
TTGTATTTAAACAATAATAAAAGTAACTTAAGTTTGCTCTATCAGATTTTAGTTCTGCACAGAGGTTAAAGTGGGAAAAATG 2614
CAGCTGTTGCAAAAATGTATATAAATAGTATGTTTCATTTTTTTCAGTATATTATCTGATACCTGTGTAGCAGCAGGTCTG 2693
CTTAAACCTAGTCTTGTGTTATTGAGTCATTTCCCTCTCCTTTGATAACTAGAACTGAAAAGCATTTTAAACATTCTTCT 2772
CCTGGAAGAAATGAATTACTTGAAGCATGAAAGACACACAGGTTGTTGTTTATTATTAGCAATTATGACTGTAGATTTA 2851

Fig. 10E

AAACAAGCAAAGAAACACACCTCAGCAGCTGCCCGTTTCCTTAGTCTCCACTTCAGAGGGGATGCCAAGAGGTCGG 2930
 CCCAGCTCCGGTGACCATGAAGGTGGCACAGGAATTACAGTGTGAATGGCTGTGTCAAGATGTTTTCGTACCTCAGATTA 3009
 AAAATATTGCTGAGGTCAGACGCCACAAATTTTCATGACTTTCATCAGAAGTAGCACATTTTCGTGACTTCCGCTGCCT 3088
 CTGAAAACAAAGTTATTGGAAACATGTTCAATGCAAAAGTGATCTGACCAAGTCATAAATCGAGCTTTTCTACTGACAT 3167
 GAACTGTTGGAAACTGATCTCATTTTATAAGAAATGATTTTCCCTCAAGGAGGCGTCTGTAAATTCAGAACAGTCCA 3246
 GACATCAGCTGTACCTCATGCTCAGTAGTTTATTATTGAGTTTCTTTTGTGAGTTAACTATGGGAGATTTAAACCTCTTT 3325
 TGCCAAAGAGGGAAGTGTGTGTTTTTTAATAGAAAAATATGACCCAAAAATTTTTTCCCTGAAGAAATGTATTATAA 3404
 CCTATTGTGTGGTTATTACATCCTGTGAAATGTATATATGTTAAAAATAATGGGGGTGCTGGAAGGTCATGGCAGACT 3483
 AGCTGCTGGTTAGTGTGGAGGGGAAGTGGTTTACTTTGTAGAGTTTACATGGTTTTATGCGGCACACACTAATTGTAAATAA 3562
 CTATGCCAAACCAATAAAAAAATAAAAAA 3594

Fig. 10F

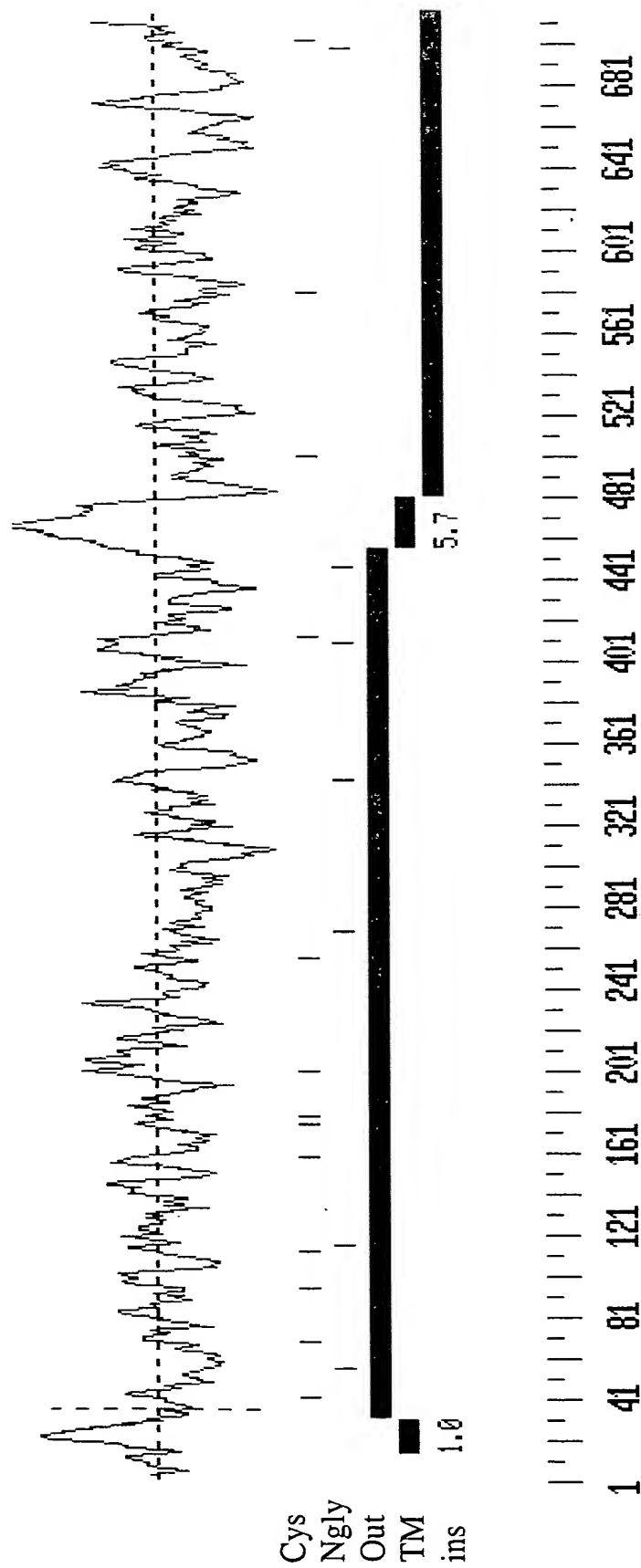


Fig. 10G

R	E	E	K	R	W	R	W	R	I	N	N	S	V	F	N	G	N	V	T	N	154
CGT	GAA	GAG	AAA	AGG	TGG	CGT	TGG	ATC	AAC	AAC	TCT	TCT	GTG	TTC	AAT	GGC	AAT	GTT	ACC	AAT	640
Q	N	Q	N	F	N	C	A	T	I	G	L	T	K	T	F	D	A	A	S		174
CAG	AAT	CAG	AAT	TTC	AAC	TGT	GCG	ACC	ATT	GGC	CTA	ACA	AAG	ACA	TTT	GAT	GCT	GCA	TCA		700
C	D	I	S	Y	R	R	I	C	E	K	N	A	K	*							188
TGT	GAC	ATC	AGC	TAC	CGC	AGG	ATC	TGT	GAG	AAG	AAT	GCC	AAA	TGA							745
TCACAGTTCCCTGTGACAAAGAACTATACTTGCAACTCTTTTGAATCCATACAGGTCGTCTGGCCCAATGATTCTTTTAC																					824
TTACCTATCTGTCTACCAAGTAGCGGTCTTGCCCATTTGGGAAACTGAGCTTCTTTCTCTGCACCTGGGGACTGGATG																					903
CTAGCCATCTCCAGGAGACAGGATCAGTTTACGGAACAACACTCAGTTAGTATAGAGATGAGGTCCGCTTCTGTAGTAC																					982
TGAGCATTTCTGACTGATCAAAAAGGCCCTAGTCTGTTGACAGGGTTTGTATTTTAGCCTCAGAGTATACCATACTA																					1061
CTAGGGAGTAACGTAGAGTGAGAAATTATAAACATTATTAGGGATTACCATTGGGAAGAGGGATAAACATAGGTCC																					1140
TGTGACTTCGTCCTCTCAAGGGAACCCCATTCACATGCCCTCCTAACTCCACAAGCGAGGGTAGCAGAGGCTCT																					1219
CCTCAGTCTGAACATAAGGCTTGGCCTTGGGAGGGCTCCTAGTCTGAGCTTGAGCAGCACGGACAGCAGCATTTGTTT																					1298
ATGGGAATGGAGAGAGGTCTGGGCAGGATAGGAACCTTCTTGGAGACCCCTTTGAAGAAAACCCAGGCAGCCAAAGGAGC																					1377
CAAAACACACTAGATTTCGTCTTCAGCAAAAGCCCTGAAGAGACACTTAAAGCTAAAATTCCTTGTCAATATTTCTGAA																					1456
ACTCCATTATAACATATGTAACTCTTTGTAAACCAAAATTTAGGTAAGCAGGCTTCTTGTCTCTGAAGGTTTGTAGTA																					1535
CCTGGCTGTATTGTGTAGTAATTTTAAATTTTGGATAGTCTCTTAGGCAACAATAATCACAATATATTCATCCCTTC																					1614
AGTTCTGGAGAAAGCCTGATACCAGGCACAGCCCTACTGACCCCAAGGAGCCTGGCAGCTGATTGGCATCACATTGATCTA																					1693
GAACTGGTCCAGCCCGCAAGAGTAGGAAAGAGAAAGGGCTGCTCAGGGAAACATTTGGCTGGGGCACGGAATAAGCAC																					1772
ATAGTAAAAGGGAACATCAGGGTCAAAATGGAAATCACCTGAGACAGGAAACAGGGAGTTTCATTTGGCCACACTGGAAG																					1851
AAAGGCAAGAAAGAGGAACAAGTCTTGGAGTACCCCTGGCTGTTCTCCACACTCAAGAACATCAGCTATACTCTGCT																					1930
TGGTGCATAAGAAAGAGAAAGAGATGCCTTTTGTGTTTGGTAAGAAATAATTAAACCATAAAGGAAGACCATGTATAA																					2009
AACTGATGGAAATAATAGTCAACCAAGTACAGCACATACCATTTTGTGTCTAATAACAATGTAGCACAGTAATGACTGT																					2088

Fig. 11B

ACATGTCAATTGTATATACCAACAAGATTGTTGTAATCATATATTTTATTACAACACTAAGTTCTGCTTCTGCATT 2167
 CCTAGGTTTTCATCATATTTTGGCTCCTTAGCATGGCCACTTACAATTTTAAACATGAGATAACACATCAGGTGTCAGAA 2246
 CTTGCTTGAAGGAATTACCAGAAGTAATTTGTGTTTGAGATGGGTGGAATTTGGAATTATATAGTAGCCGGTGGAG 2325
 ATACAAGTTCCTGACTGTGTTGGGAAAAGGATAAGTGCTACCGTTGAGAAGGGAAGAAAGGCTGAGTCTAGGTGGAGAA 2404
 AAATATCAACAGAACTCTAGCCAAAGGCAAGCCAGAACTCAGACAAACAGAAAGGAATCCTAATCCTTCTGTTTGA 2483
 GAAGAGAACTGTAGTTGCTTCACTTCTATTTTCATGACAGATAAAGTCAAACTTTTAAAGATCAGGAAATGTAGACA 2562
 TCTAGTGATTTCTTGTAGACAGATTAAATTTCCCCAAGATTAGGAGACACTTCTGTGCAAGTTCTTAAAGTTCCTGGA 2641
 ATGGCCTGGGTGGGAGTAGATAGGGAATATGTGGGATTTGGTTTAAAGTTTCATCATTTGGGAGAGTTCCCTGGA 2720
 TCCCTTGCAAGCTTAGATAAATGTGATCTTTATTAGATAGCAGTGGCATGCTTTTAAAAAAAAGGCAATGAAAAATTA 2799
 GCAAGCCACTGAATTTGAGTTTTCACCTTGTTCATATGCTGTGTAATCAGTACAGTTTCTTACCCCTTCTTGGT 2878
 CTTAAATTTCCCTACTGATAAAATGGGGTAGTAATACCTATCTCAAAAAATTAATGCACATATTAATAACATTCCTCTA 2957
 TGTATCTCAATGGCATTAGACATTAGGAGAACATTTTGTGGAGGATTTGAAGTTGAGATCTTTCATCCAAAGAGTAGCT 3036
 TTTCAATTTGCTAGAACCTTAATGTAGGCAAGCCACTTCAATTTTTCAGAACTTGTTTACTCATTTATAATATGGGAATA 3115
 AAAATTTGTGCAAGTCAGAGAAAGGTGCCCTTAAAAATGTTGTGGCCAAAGCCACATGAGATCAAAGACACACTTTTCATG 3194
 ACCTCAAATGTGGCCAGCCTAGGTCAGCCCAACCCCATCCAAACCTTAGACTCACGAACAAATCCACCTGAGATCAG 3273
 CAGAGCCACCCTAGATCAGCTGAAACTCTAAGCACAAAAATAAAACTTATCACTGTAAAAAAAATAAAATAAA 3352
 GTCTCTCGTATAGCAAAATCTAACTGATGCAATCTCCATCTGGCCCTTCATCCTTCTCCCTTTATTTGTCCTTTTCGTGTAT 3431
 TGTTCATCCAGCAACCAGGATGATCTTTGTTAAAAACATTAACACAGATTCTGTCAATCTTTMAAAAAATAAAAGCCATGA 3510
 AATTNTAGCAAGCCACTGAATTTGAGTTTTCACCTTGGTTTCTAATAATGCTGTGTAATCAGANCAGKTTTCTTACCCT 3589
 TTCTTGGTCTTAATTTCTACTGATAAAATGGGTGWTGTAATACCTATCTCAAAAAATTAATGACACATATTARATAACA 3668
 TTCCTCTATGTATCTCAATGGCATTAGACATTAGGAGAAGCATTTTGTGGAGGATTTGAAGTTGAGATCTTCATCCCAAG 3747
 AAGTAGCTTTTCAATTTGTSTAGAAGCTTAATGTAGGCAAGCCACTTCATTTTTCAGAACTTGTTTACTCATTTTATAATA 3826
 TGGGAATAAAAAATTTGTGCAAGTCAGAGAAGGTGCCCTTAAAAAATGTTGTGGCCAAAGCCACATGAGATCAAAGACACAC 3905
 TTTTTCATGACCTCAAAATGTGGGCCAGCCTAGGTCAGCCCAACCCCATCCACCTTAGACTCACGAACAAATCCACCT 3984
 GAGATCAGCAGAGCCACCTAGATCAGCTGAACCTCTAAGCACAAAAATAAAACTTATCTACTGTAAAAATAAAAAAA 4063
 AAAAAAAGAA 4074

Fig. 11C

GTGGTCGGCGGAGGTGAGACTGTGAAGAAGGAACGTTGCTTGGCAAAAGGAGCATATTTCTCAGGAGACGGGC	79
CCCTGCCTGCCACACCAAGCATTAGGCCACCAGGAAGACCCCCATCTGCAAGCAAGCCTAGCCTTCCAGGGGAGAAAGAG	158
<div style="text-align: center;"> M N W H M I I S G L I V V V </div>	
GCCCCCTGCAGCTCCTTCATC ATG AAC TGG CAC ATG ATC ATC TCT GGG CTT ATT GTG GTA GTG	14 220
L K V V G M T L F L L Y F P Q I F N K S	34
CTT AAA GTT GTT GGA ATG ACC TTA TTT CTA CTT TAT TAT TTC CCA CAG ATT TTT AAC AAA AGT	280
N D G F T T T R S Y G T V S Q I F G S S	54
AAC GAT GGT TTC ACC ACC ACC AGG AGC TAT GGA ACA GTC TCA CAG ATT TTT GGG AGC AGT	340
S P S P N G F I T T R S Y G T V C P K D	74
TCC CCA AGT CCC AAC GGC TTC ATT ACC ACA AGG AGC TAT GGA ACA GTC TGC CCC AAA GAC	400
W E F Y Q A R C F F L S T S E S S W N E	94
TGG GAA TTT TAT CAA GCA AGA TGT TTT TTC TTA TCC ACT TCT GAA TCA TCT TGG AAT GAA	460
S R D F C K G K G S T L A I V N T P E K	114
AGC AGG GAC TTT TGC AAA GGA AAA GGA TCC ACA TTG GCA ATT GTC AAC ACG CCA GAG AAA	520
L K F L Q D I T D A E K Y F I G L I Y H	134
CTG AAG TTT CTT CAG GAC ATA ACT GAT GCT GAG AAG TAT TTT ATT GGC TTA ATT TAC CAT	580

Fig. 11D

R	E	E	K	R	W	R	W	I	N	N	S	V	F	N	G	K	Y	V	N	154
CGT	GAA	GAG	AAA	AGG	TGG	CGT	TGG	ATC	AAC	AAC	TCT	GTG	TTC	AAT	GGC	AAG	TAC	GTG	AAC	640
M	P	Q	F	P	G	D	L	G	L	L	Q	K	T	K	P	E	I	A	G	174
ATG	CCA	CAG	TTT	CCT	GGG	GAT	CTT	GGT	TTG	CTT	CAA	AAG	ACC	AAA	CCT	GAG	ATT	GCT	GGG	700
F	T	L	E	*																178
TTC	ACC	CTG	GAA	TAG																715
CTCAA	ACGCTGACACTTGACTCTGTTCTGCTCTTCTCCTTCTTCTTCCA	ACCCATCTATTCCCTATCTGTCTACCAGTAGC	794																	
GGTCC	TGCCCATTTGGGAAACTGAGCTTCTTCTCTGCACTGGGGACTGGATGCTAGCCATCTCCAGGACAGGA	873																		
TCAGT	TTTACGGAACAACCTCAGTTAGTATAGAGATGAGGTCGGCTTCTGTAGTACTGAGCATTTCTGACTGATCAAAA	952																		
AGGC	TAGTCTGTTGACAGGGTTTGTATTTTAGCCTCAGAGTATACCATACTACTAGGGAGTAACGTAGAGTGAG	1031																		
AAATT	TATAAACATTTTAGGGATTACCATGGTGGAGAGGGATAAACATAGGTCCCTGTGACTTCGTCTCTGTCTCAA	1110																		
GGGA	ACCCCATTCACATGCCCTCCTAACCTCCACAAGCGAGGGTAGCAGAGGCTCTCCTCAGTCTGAACTAAGGCTTGG	1189																		
CCTT	GGGAGGGCTCCTAGTGTGAGCTTGGAGCAGCACGGACAGCATTTGTTATGGGAATGGAGAGAGGCTGGG	1268																		
CAGGA	TAGGAACCTTCTTGGAGACCCCTTTGAAGAAACAGGCAGCCAAGGAGCCAAACACACTAGATTTCTGTTCT	1347																		
TCAGC	AAAGCCCTGAAGACACTTAAAGCTAAAAATTCCTTGTCTATATTTCTGAAACTCCATTATAACATATGTAACT	1426																		
CCTT	TGTAACCAAAATTTAGGTAGCAGGCTTCCTTTGCTCTGAAGTTTGTAGTACCCTGGCTGTATTTGTGAGTATT	1505																		
TTTAA	AAATTTTGGATAGTCTCTTAGGCAACAATAATCACAATATATTTCATCCCTTCAGTCTCTGGAGAAAGCCTGATACC	1584																		
AGGC	CACGCTACTGACCCCAAGGAGCCTGGCACTGATTGGCATCACATTTGATCTAGAACTGGTCCAGCCCGCGAAGAG	1663																		
TAGG	AAAAGAGAGAGGGCTGCTCAGGGAAACATTGGCTGGGGCCACGGAATAAGCACATAGTAAAAAGGGAACATCAGGG	1742																		
TCAA	ATGGAAATCACCTGAGACAGGAAACAGGGAGTTCAATTTGGCCACACTGGAAGAAAGCAAGAAAGAGAACAA	1821																		
GTC	TGGAGTACCCCTGGCTGTTCTCCACACTCACAAGACATCAGCTATACTCTGCTTGGTGCATAAGAAAGAGAAAAAGA	1900																		

Fig. 11E

GATGCC	1979
TTTGTG	2058
TTTGTG	2137
TTTGTG	2216
TTTGTG	2295
TTTGTG	2374
TTTGTG	2453
TTTGTG	2532
TTTGTG	2611
TTTGTG	2690
TTTGTG	2769
TTTGTG	2848
TTTGTG	2927
TTTGTG	3006
TTTGTG	3085
TTTGTG	3164
TTTGTG	3243
TTTGTG	3322
TTTGTG	3401
TTTGTG	3480
TTTGTG	3559
TTTGTG	3638
TTTGTG	3717

Fig. 11F

AGCTTAATGTAGGCAAGCCACTTCATTTTTCAGAACTTGTTTACTCATTTTATAATATGGGAATAAAAAATTTGTGCAAAGT 3796
CAGAGAAAGGTGCCCTTAAAAAATGTTGTGGCCCAAGCCACATGAGATCAAAGACACACACTTTTTCATGACCTCAAAATGTGGGC 3875
CCAGCCTAGGTCAGCCCAACCCCCCATCCAAACCCTTAGACTCACGAAACAAATCCACCTGAGATCAGCAGAGCCACCCCTAGA 3954
TCAGCTGAAACTCTAAGCACAAAAAATAAAAACTTATCACTGTAAAAAATAAAAAAATAAAAAA 4018

Fig. 11G

GAGACTGTGAAGAAGAAACGTTGCTTGGGCAAAAGGAGCATATTTCTCAGGAGACGGGGCCCCCTGCCCTGCCACACCA	79
AGCATTAGGCCACCCAGGAAGACCCCCCATCTGTCAAGCAAGCCTAGCCTTCCAGGGAGAAAGAGGCCCTTGCAGCTCCTTC	158
<div> <div>M</div> <div>N</div> <div>W</div> <div>H</div> <div>M</div> <div>I</div> <div>I</div> <div>S</div> <div>G</div> <div>L</div> <div>I</div> <div>V</div> <div>V</div> <div>V</div> <div>L</div> <div>K</div> <div>V</div> <div>V</div> <div>G</div> </div>	19
ATC ATG AAC TGG CAC ATG ATC ATC TCT GGG CTT ATT GTG GTA GTG CTT AAA GTT GTT GGA	218
<div> <div>M</div> <div>T</div> <div>L</div> <div>F</div> <div>L</div> <div>L</div> <div>L</div> <div>Y</div> <div>F</div> <div>P</div> <div>Q</div> <div>I</div> <div>F</div> <div>N</div> <div>K</div> <div>S</div> <div>N</div> <div>D</div> <div>G</div> <div>F</div> <div>T</div> </div>	39
ATG ACC TTA TTT CTA CTT TAT TAT TTC CCA CAG ATT TTT AAC AAA AGT AAC GAT GGT TTC ACC	278
<div> <div>T</div> <div>T</div> <div>R</div> <div>S</div> <div>S</div> <div>Y</div> <div>G</div> <div>T</div> <div>V</div> <div>C</div> <div>P</div> <div>K</div> <div>D</div> <div>W</div> <div>E</div> <div>F</div> <div>Y</div> <div>Q</div> <div>A</div> <div>R</div> <div>C</div> </div>	59
ACC ACC AGG AGC TAT GGA ACA GTC TGC CCC AAA GAC TGG GAA TTT TAT CAA GCA AGA TGT	338
<div> <div>F</div> <div>F</div> <div>L</div> <div>S</div> <div>T</div> <div>S</div> <div>E</div> <div>S</div> <div>S</div> <div>W</div> <div>N</div> <div>E</div> <div>S</div> <div>R</div> <div>D</div> <div>F</div> <div>C</div> <div>K</div> <div>G</div> <div>K</div> </div>	79
TTT TTC TTA TCC ACT TCT GAA TCA TCT TGG AAT GAA AGC AGG GAC TTT TGC AAA GGA AAA	398
<div> <div>G</div> <div>S</div> <div>T</div> <div>L</div> <div>A</div> <div>I</div> <div>V</div> <div>N</div> <div>T</div> <div>P</div> <div>E</div> <div>K</div> <div>L</div> <div>L</div> <div>K</div> <div>F</div> <div>L</div> <div>Q</div> <div>D</div> <div>I</div> <div>T</div> </div>	99
GGA TCC ACA TTG GCA ATT GTC AAC ACG CCA GAG AAA CTG AAG TTT CTT CAG GAC ATA ACT	458

Fig. 11H

D	A	E	K	Y	F	I	G	L	I	Y	H	R	E	E	K	R	W	R	W	119
GAT	GCT	GAG	AAG	TAT	TTT	ATT	GGC	TTA	ATT	TAC	CAT	CGT	GAA	GAG	AAA	AGG	TGG	CGT	TGG	518
I	N	N	S	V	F	N	G	N	V	T	N	Q	N	Q	N	F	N	C	A	139
ATC	AAC	AAC	TCT	GTG	TTC	AAT	GGC	AAT	GTT	ACC	AAT	CAG	AAT	CAG	AAT	TTC	AAC	TGT	GCG	578
T	I	G	L	T	K	T	F	D	A	A	S	C	D	I	S	Y	R	R	I	159
ACC	ATT	GGC	CTA	ACA	AAG	ACA	TTT	GAT	GCT	GCA	TCA	TGT	GAC	ATC	AGC	TAC	CGC	AGG	ATC	638
C	E	K	N	A	K	*														165
TGT	GAG	AAG	AAT	GCC	AAA	TGA														659
TCACAGT	TCCCCTGTGACAAGAACTATACTTGC	AACTACTTTTGAATCCATACAGGTCG	TCCTGGCCAATGATCTTTTAC	738																
TTACCTAT	CTGTCTACCAAGTAGCGGTCCTTGCCCA	TTTGGAAACTGAGCTTCTTCTCTGCACT	GGGACTGGGATG	817																
CTAGCCAT	CTCCAGGAGACAGGATCAGTTTACGGAA	ACAACACTCAGTTAGTATAGAGATGAGGT	CCGCTTCTGTAGTAC	896																
TGAGCAT	TTCTGACTGATCAAAAAGGCCTAGTCTGT	TTGACAGGGTTTGTTTATTATTAGCCTCAG	AGTATACCATACTA	975																
CTAGGGAG	TAACTGTAGAGTGAGAAATTATAAACAT	TATTAGGGATTACCATGGTGGAGAGGGATAA	ACATAGGTCC	1054																
TGTGACT	TCGTCCTGTCTCAAGGGAACCCCATTCAC	ATGCCCTCCTAACTCCACAAGCGAGGTAGC	AGGCTCT	1133																
CCTCAGT	CTGAACATAAGGCTTGCCCTTGGGAGGG	CTCCTAGTGTGAGCAGCACGGACAGCAGCAT	TGTTT	1212																
ATGGGA	ATGGAGAGAGGTCTGGGCAGGATAGGAAC	CTTCTTGAGACCCCTTTGAAGAAACCCAGG	CAGCCAAAGGAGC	1291																
CAACACAC	TAGATTCTGTCTTCAGCAAAAGCCCTGA	AGACACTTAAGCTAAAATTCCTTGTCA	TATTTCTGAA	1370																
ACTCCAT	TATAACATATGTAACTCCTTTGTAA	CCAAAATTTAGGTAAGCAGGCTTCCTTT	GTCTGAAAGTTT	1449																
CCTGGC	TGTAATTTGTGAGTATTTTAAATTTT	GGATAGTCTCTTAGGCAACAATAATCACA	TATATTCATCCCTC	1528																
AGTTCT	GGAAAGCCCTGATACCAGGCACAGCC	TACTGACCCCAAGGAGCCTGGCACTGAT	TGGCATCACAT	1607																

Fig. 11I

GAACTGGTCCAGCCGCGAAGAGTAGGAAAAGAGAAGGGCTGCTCAGGGAAACATTTGGCTGGGGCACGGAAATAAGCAC 1686
 ATAGTAAAAAGGGAACATCAGGGTCAAAATGGAAAATCACCTGAGACAGGAAACACAGGAGTTTCATTTGGCCACACACTGGAAG 1765
 AAAGGCAAGAAAGAGGAAGACAAGTCTTGGAGTACCCCTGGCTGTTCTCCACACTCACAAGACATCAGCTATACTCTGCT 1844
 TGGTGCAATAAGAAAAGAGAAAAGAGATGCCTTTTGTGTTTGTAGTAAGAATAATTAACCCATAAGGAAGACCATGTATAA 1923
 AACTGATGGAAATAATAGTCAACCAAAAGTACAGCACATACCATTTTGTGTCTAATAACAATGTAGCACAGTAATGACTGT 2002
 ACATGTCATTGTATGTATACCAAAACAAGATTGTTGTGTAATCATATTTTATTATTAACAACACTAAAGTTCGTCTCTGCATT 2081
 CCTAGGTTTCATCATTTTGGCTCCTTAGCATGGCCACTTACAATTTTTTAACATGAGATAACACATCAGGTGTCAGAA 2160
 CTTGCTTGAAGGGAATTACCAGAAAGTAATTTGTGTTTGAGATGGGTGGAAATTGGAATTATATTAGTAGCCGGTGGAG 2239
 ATACAAGTTCTCTGACTGTGTTGGGAAAGGATAAGTGCTACCGTTGAGAAGGGAAGAAAGGCTGAGTCTAGGTGGAGAA 2318
 AAATATCAACAGAACTCTAGCCAAAGGCAAGCCCCAGAACTCAGACAAACAGAAAAGGAAATCCTAATCCTTCTGTTTGA 2397
 GAAGAGAGAACTGTAGTTGCTTCACCTTCCTATTTCATGACAGAAATAACTGCAAACTTTTAAGATCAGGAAAATGTAGACA 2476
 TCTAGTGATTTCTTTAGTAGACAGATTTAATTTCCCCCAAGATTAGGAGACACTTCTGTGCAGGTTCTAAAAAGGAGCCCA 2555
 ATGGCCCTGGGTGGGAGTAGATAGGGAATATGTGGGATTTTGGTTTAAAGTTTCATCATTTGGGAGAGTTCCTGGA 2634
 TCCTTGCAAGCTTAGATAAATGTGATCTTTATTAGATAGCAGTGGCATGCTTTTAAAAAAGGCAATGAAAAATTTA 2713
 GCAAGCCACTGAATTTGAGTTTTCACTTTGTCTTAATAATGCTGTGTGAATCAGTACAGTTTTCCTTACCCCTTCTTGGT 2792
 CTTAATTTCCCTTACTGATAAAAATGGGTAGTAATACTATCTCAAAAAATTAATTGCACATATTAAATAACATTCCCTCTA 2871
 TGTATCTCAATGGCATTAGACATTAGGAGAAAGCATTTTGTGGAGGATTTGAAGTTGAGATCTTCATCCAAGAAGTAGCT 2950
 TTTCAATTTGCTAGAAGCTTAATGTAGGCAAGCCACTTCATTTTTCAGAACTTGTGTTTACTCATTTATATAATATGGGAATA 3029
 AAAATTTGTGCAAGTCAGAGAAAGGTGCCCTTAAAAATGTTGTGGCCCAAGCCACATGAGATCAAAGACACACTTTTCATG 3108
 ACCTCAAATGTGGGCCAGCCTAGGTCAGCCAAACCCCATCCACCTTAGACTCACGAACAAATCCACCTGAGATCAG 3187
 CAGAGCCACCCCTAGATCAGCTGAAACTCTAAGCACAAAAATAAAACCTTATCAGTAAAAAATAAAAAAATAAAAAA 3266
 GTCTCTCGTATAGCAAAAATCTAACTGATGCAATCTCCATCTGGCCTTCATCCTTCTCCCTTTTATTGTCCTTTCGTGTAT 3345
 TGTTCATCCAGCAACCAGGATGATCTTGTGTTAAAAACATTAAACAGATTCTGTCAYKCTTMAAAAAAATAAGCCATGA 3424
 AATTNTAGCAAGCCACTGAATTTGAGTTTTCACTTTGGTTTCTAATAATGCTGTGTAATCAGANCAGKTTTCTTACCCT 3503

Fig. 11J

TTCTTGGTCTTAATTTCCTTACTGATAAAATGGGGTGWGTAATAACCTATCTCAAAAAAATTATTGCACATATTARATAACA 3582
TTCCTCTATGTATCTCAATGGCAATTAGACATTAGGAGAAAGCATTTTGTGGAGGATTTTGAAGTTGAGATCTTCATCCAAG 3661
AAGTAGCTTTTCAATTTGSTAGAAGCTTAAATGTAGGCAAGCCACTTCATTTTTCAGAACTTGTTACTCATTTATAATA 3740
TGGGAATAAAAAATTTGTGCAAGTCAGAGAAGGTGCCCTTAAAAATGTTGTGGCCAAAGCCACATGAGATCAAAAGACACAC 3819
TTTTCATGACCTCAAATGTGGGCCCAGCCTAGGTCAGCCCAACCCCCATCCAAACCTTAGACTCACGAACAAATCCACCT 3898
GAGATCAGCAGAGCCACCCCTAGATCAGCTGAAACTCTAAGCACAAAAATAAAAACTTATCACTGTAAAAAATAAAAAA 3977
AAAAAAA 3985

Fig. 11K

GAGACTGTGAAGAAGAAACGTTGCTTGGGCAAAAGGAGCATATTCTCAGGAGACGGGGCCCCCTGCCCTGCCACACCA	79
AGCATTAGGCCACCAGGAAGACCCCCCATCTGCAAGCAAGCCTAGCCTTCCAGGGAGAAAAGAGGCCCTGCAGCTCCTTC	158
M N W H M I I S G L I V V V L K V V G ATC ATG AAC TGG CAC ATG ATC ATC TCT GGG CTT ATT GTG GTA GTG CTT AAA GTT GTT GGA	19 218
M T L F L L Y F P Q I F N K S N D G F T ATG ACC TTA TTT CTA CTT TAT TTC CCA CAG ATT TTT AAC AAA AGT AAC GAT GGT TTC ACC	39 278
T T R S Y G T V C P K D W E F Y Q A R C ACC ACC AGG AGC TAT GGA ACA GTC TGC CCC AAA GAC TGG GAA TTT TAT CAA GCA AGA TGT	59 338

Fig. 11L

[illegible]

Fig. 11M

CCTTTGTAACCAAAATTTAGGTAAGCAGGCTTCCTTTGCTCTGAAGGTTTGTAGTACCTGGCTGTATTTGTTGAGTATT 1419
 TTTAAAAATTTTGGATAGTCTCTTAGGCAACAATAATCACAAATATATTTCATCCCTTCAGTTCTGGAGAAAAGCCTGATACC 1498
 AGGCACAGCCTACTGACCCCAAGGAGCCTGGCACTGATTGGCATCACATTTGATCTAGAACTGGTCCAGCCGCCGAAGAG 1577
 TAGGAAAAGAGAAAGGGCTGCTCAGGGAAACATTTGGCTGGGGCACGGAATAAGCACATAGTAAAAAGGGAACATCAGGG 1656
 TCAAAATGGAAATCACCTGAGACAGGAAACAGGGAGTTTCATTTGGCCACACTGGAAAGAAAGCAAGAAAGAGGAAGACAA 1735
 GTCCTTGGAGTACCCCTGGCTGTTCTCCACACTCAAGACATCAGCTATACTCTGCTTGGTGCTATAAGAAAGAGAAAAAGA 1814
 GATGCCCTTTTGTGTTTGTAGTAAGAAATAATTAAACCATAAGGAAGACCATGTATAAAACTGATGGAAATAATAGTCACC 1893
 AAAGTACAGCACATACCATTTTGTGCTTAATAACAATGTAGCACAGTAATGACTGTACATGTCTCATTTGTATGTATACCAA 1972
 ACAAGATTGTTGTAATCATATTTTATTATTAACAACACTAAGTTCTGCTTCTGCATTCCTAGGTTTCATCATTTTGTGGCT 2051
 CCTTAGCATGGCCACTTACAAATTTTTTAACATGAGATAACACATCAGGTGTCAGAACTTGCTTGAAGGGAATTACCAGA 2130
 AGTAAATTTGTGTTTGAGATGGGTGGAATTTGGAATTATATTAGTAGCCGGTGGAGATACAAGTTCTCTGACTGTGTTG 2209
 GGAAGGATAAGTGCTACCCGTTGAGAAAGGAAAGGCTGAGTCTAGGTGGAGAAAAAATATCAACAGAACTCTAGCCCA 2288
 AAGGCAAGCCCCAGAACTCAGACAACTAGCAAAATCCTAATCCTTCTGTTTGTGAGAAAGAGAACTGTAGTTGCTTC 2367
 ACTTCCATTTTTCATGACAGAAATACTGC AAACTTTTAAGATCAGGAAATGTAGACATCTAGTGATTTCTTTAGTAGACA 2446
 GTTTAAATTTCCCCCAAGATTAGGAGACACTTCTGTGCAGGTTCTAAAAAGGAGCCCAATGGCCCTGGGGTGGAGTGGGGA 2525
 GTAGATAGGGAAATATGTGGGATTTGGTTTAAAGTTTCATCATTTGGGAGAGTTCCCTGGATCCTTGCAAGCTTAGATAAATGT 2604
 GATCTTTTATTAGATAGCAGTGGCATGCTTTTAAAAAAAAGGCAATGAAAAATTTAGCAAGCCCACTGAATTTGAGTTT 2683
 CACTTTGTTTCTAATATGCTGTGTAATCAGTACAGTTTCTTACCCCTTCTTGGTCTTAATTTCCCTTACTGATAAAAT 2762
 GGGGTAGTAATACCTATCTCAAAAATTTATTGCACATATTAAAAACAATTCCTCTATGTATCTCAATGGCATTAGACAT 2841
 TAGGAGAAAGCATTTTGTGGAGGATTTGAAGTTGAGATCTTCATCCAAAGTAGCTTTTCAATTTGCTAGAAGCTTAAT 2920
 GTAGGCAAGCCACTTCAATTTTCAGAACTTGTTTACTCATTTATAATATGGGAATAAAAAATTTGTGCAAGTCAGAGAAG 2999
 GGTGCTTAAAAAATGTTGTGGCCAAGCCACATGAGATCAAGACACACTTTTTCATGACCTCAAAATGTGGGCCCCAGCCTA 3078
 GGTACGCCAACCCCAATCCCTTAGACTCACGAAACAAATCCACCTGAGATCAGCAGAGCCACCCCTAGATCAGCTGA 3157
 AACTCTAAGCACAAAAATAAAACTTATCACTGTAAAAAAAATAAAAGTCTCTCGTATAGCAAAAATCTAA 3236

Fig. 11N

CTGATGCAATCTCCATCTGGCCTTTCATCCCTTCTCCCTTTATTTGTCCCTTTCGTGTATTTGTTTCATCCAGCAACCAGGATGA 3315
 TCTTGTATAAACACATTAAACAGATTCTGTCAWKCTTTMAAAAAAAGCCCATGAAATTNTAGCAAGCCACTGAATTT 3394
 GAGTTTTCACCTTTGGTTTCTAAATATGCTGTGTGAATCAGANCAGKTTTCTTACCCCTTTCTTGGTCTTAATTTCCCTTACT 3473
 GATAAAATGGGTTWGTAATACCTATCTCAAAAAAATATTGCACATATTARATAACATTCCCTCTATGTATCTCAATGGCA 3552
 TTAGACATTAGGAGAAGCAATTTGTGGAGGATTTTGAAGTTGAGATCTTCATCCCAAGAAGTAGCTTTTCAATTTGSTAGA 3631
 AGCTTAATGTAGGCAAGCCACTTCATTTTTCAGAACTTGTTTACTCATTTATAATATGCGAATAAAAAATTTGTGCAAGT 3710
 CAGAGAAAGGGTGCCTTAAAAATGTTGTGGCCCAAGCCACATGAGATCAAGACACACACTTTTCATGACCTCAAAATGTGGGC 3789
 CCAGCCTAGGTCAGCCAAACCCCATCCACCTTAGACTCACGAAACAAATCCACCTGAGATCAGCAGAGCCACCCCTAGA 3868
 TCAGCTGAAACTCTAAGCACAAAAAATAAAAACTTATCACTGTAAAAAATAAAAAAAGAAAGCAACCTGCCCCG 3947

Fig. 110

GAGACTGTGAAGAAGAAACGTTGCTTGGGCAAAAGGAGCATATTCTCAGGAGACGGGGCCCCCTGCCCTGCCACACCA	79
AGCATTAGGCCACCCAGGAAGACCCCCCATCTGCAAGCAAGCCTAGCCTTCCAGGGAGAAAGAGCCCCCTGCAGCTCCTTC	158
M N W H M I I S G L I V V V L K V V G	19
ATC ATG AAC TGG CAC ATG ATC ATC TCT GGG CTT ATT GTG GTA GTG CTT AAA GTT GTT GGA	218
M T L F L L Y F C P K D W E F Y Q A R C	39
ATG ACC TTA TTT CTA CTT TAT TTC TGC CCC AAA GAC TGG GAA TTT TAT CAA GCA AGA TGT	278
F F L S T S E S S W N E S R D F C K G K	59
TTT TTC TTA TCC ACT TCT GAA TCA TCT TGG AAT GAA AGC AGG GAC TTT TGC AAA GGA AAA	338

Fig. 11P

G	S	T	L	A	I	V	N	T	P	E	K	L	K	F	L	Q	D	I	T	79
GGA	TCC	ACA	TTG	GCA	ATT	GTC	AAC	ACG	CCA	GAG	AAA	CTG	AAG	TTT	CTT	CAG	GAC	ATA	ACT	398
D	A	E	K	Y	F	I	G	L	I	Y	H	R	E	E	K	R	W	R	W	99
GAT	GCT	GAG	AAG	TAT	TTT	ATT	GGC	TTA	ATT	TAC	CAT	CGT	GAA	GAG	AAA	AGG	TGG	CGT	TGG	458
I	N	N	S	V	F	N	G	N	V	T	N	Q	N	Q	N	F	N	C	A	119
ATC	AAC	AAC	TCT	GTG	TTC	AAT	GGC	AAT	GTT	ACC	AAT	CAG	AAT	CAG	AAT	TTC	AAC	TGT	GCG	518
T	I	G	L	T	K	T	F	D	A	A	S	C	D	I	S	Y	R	R	I	139
ACC	ATT	GGC	CTA	ACA	AAG	ACA	TTT	GAT	GCT	GCA	TCA	TGT	GAC	ATC	AGC	TAC	CGC	AGG	ATC	578
C	E	K	N	A	K	*														145
TGT	GAG	AAG	AAT	GCC	AAA	TGA														599
TCACAGT	TCCCTGTGACAA	GAAC	TATAC	TGCA	ACTCTTTT	TGAA	TCCATACAGG	TCGTCTGGCC	CAATGAT	TCTTTTAC										678
TTACCTA	TCTGTCTACAG	TAGCGG	TCCCTTG	GGAA	AACTGAGC	TTCTTCTCTG	CAC	TGGG	ACTGGG	GACTGGG	ATG									757
CTAGCCAT	CTCCAGGAGAC	GAGATCAG	TTTACG	GAAACAACTCAG	TTAGTATAGAG	ATGAGTCCG	CTTCTGTAGTAC													836
TGAGCA	TTTCTGACTGATCA	AAAAGGCC	TAGTCTGT	TGACAGG	TTTGTATTTTAG	CCCTCAGAGT	ATACCAT													915
CTAGGGAG	TAACTGTAGAG	TGAGAA	ATTATA	AAACAT	TATTTAGG	GATTACCAT	TGTTGGA	AGAGG	GATAA	ACATAGG	TCC									994
TGTGACT	TCGTCTGTCTCA	AGGGAACCC	ATTACAT	TGCCCC	CTCCTAACT	CCACAGC	AGGAGG	GTAGC	AGAGG	CTCT										1073
CCTCAG	CTGAAC	TAAGC	TTGGC	CTTGGG	GAGGCTCCTAG	TGCTGAGC	TTGGAG	CACG	CACG	CAGCAT	TGTTT									1152
ATGGA	ATGGAGAGG	TC	TGGCAG	GATAGG	AAACCTTCT	TGGAG	ACCCCTTT	TGA	AGAA	AAAC	CAGC	AGC	CAAGG	GAGC						1231

Fig. 11Q

CAAACACACTAGATTTCTGTCTTTCAGCAAAGCCCTGAAGAGACACTTAAGCTAAAAATTCCTTGTTCATATTTCTGTGAA
 1310
 ACTCCATTATAACATATGTAACTCCTTTGTGTAAACCAAAATTTAGGTAAGCAGGCTTCCTTTTGCTCTGAAGGTTTTTGAGTA
 1389
 CCTGGCTGTATTTTGTGAGTATTTTAAAAATTTTGGATAGTCTCTTAGGCAACAATAATCACAATATATTTCATCCCCTTC
 1468
 AGTTCTGGAGAAAAGCCCTGATACCAGGCACAGCCCTACTGACCCCAAGAGCCTGGCACTGATTGGCATCACATTGATCTA
 1547
 GAACTGGTCCAGCCGCCGAAGAGTAGGAAAAGAGAAGGGCTGCTCAGGGAAACATTGGCTGGGGCCAGGAATAAGCAC
 1626
 ATAGTAAAAAGGGAAACATCAGGGGTCAAATGGAAATCACCTGAGACAGGAAAACAGGGAGTTCAATTGGCCACACTGGAAG
 1705
 AAAGGCAAGAAAGAGGAAGACAAAGTCTTGGAGTACCCCTGGCTGTTCTCCACACTCACAAGACATCAGCTATACTCTGCT
 1784
 TGGTGCTAAAGAAAAGAGAAAGAGATGCCCTTTTGTGTTTGTAGTAAGAAATAATTAAACCATAAAGGAAGACCATGTATAA
 1863
 AACTGATGGAAATAATAGTCAACCAAGTACAGCACATACCATTTTGTGTCATAATAACAATGTAGCACAGTAATGACTGT
 1942
 ACATGTCATTGTATGTATACCAAAACAAGATTGTTGTAATCATATTTTATTACAACACTAAAGTTCTGCTTCTGCATT
 2021
 CCTAGGTTTCATCATTTTGGCTCCTTAGCATGGCCACTTACAATTTTAAATGAGATAACACATCAGGTGTCAGAA
 2100
 CTTGCTTGAAAGGGAATTACCAGAAAGTAAATTGTGTTTGTAGATGGGTGGAAATTGGAATTATATTAGTAGCCGGTGGAG
 2179
 ATACAAAGTTCTGACTGTGTTGGGAAAGGATAAGTGCTACCGTTGAGAAAGGGAAGAAAGGCTGAGTCTAGGTGGAGAA
 2258
 AAATATCAACAGAACTCTAGCCAAAGGCAAGCCCAAGAACTCAGACAAACAGAAAGGAAATCCTAATCCTTCTGTTTGA
 2337
 GAAGAGAAACTGTAGTTGCTTCACTTCCCTATTTCATGACAGAAATAACTGCAAAACCTTTTAAGATCAGGAAAATGTAGACA
 2416
 TCTAGTGATTTCTTTAGTAGACAGTTTAAATTTCCCCCAAGATTAGGAGACACTTCTGTGCAGGTTCTAAAAAGGAGCCCA
 2495
 ATGGCCCTGGGTGGGAGTGGGAGTAGATAGGGAATATGTGGGATTGTTTAAAGTTCAATTTGGGAGAGTTCCCTGGA
 2574
 TCCTTGCAAGCTTAGATAAATGTGATCTTTATTAGATAGCAGTGGCATGCTTTTAAAAAAAAGGCAATGAAAAATTTA
 2653
 GCAAGCCACTGAAATTTGAGTTTTCACCTTTGTTTCTAAATATGCTGTGTAATCAGTACAGTTTTCCTTACCCTTTCTTGGT
 2732
 CTTAAATTTCCCTTACTGATAAAAATGGGTAGTAATACCTATCTCAAAAAATATATGCACATATTAATAACATTCCCTCTA
 2811
 TGTATCTCAATGGCATTAGACATTAGGAGAAGCAATTTTGTGGAGGATTTGAAGTTGAGATCTTCATCCCAAGAAGTAGCT
 2890
 TTTCAATTTGCTAGAAGCTTAATGTAGGCAAGCCACTTCATTTTTCAGAACTTGTTTACTCATTTATAATAATGGAATA
 2969
 AAAATTTGTGCAAGTCAGAGAAGGGTGCCCTTAAAAATGTTGTGGCCCAAGCCACATGAGATCAAGACACACTTTTCATG
 3048
 ACCTCAAATGTGGGCCAGCCTAGGTCAGCCCAACCCCATCCCTTAGACTCACGAAACAAATCCACCTGAGATCAG
 3127

Fig. 11R

CAGAGCCACCCCTAGATCAGCTGAAACTCTAAGCACAAAATAAAAACTTATCACTGTAAAAAATAAAAAA
 3206
 GTCTCTCGTATAGCAAAAATCTAACTGATGCAATCTCCATCTGGCCTTCATCCTTCTCCCTTTATTGTCCTTTTCGTGTAT
 3285
 TGTTCATCCAGCAACCAGGATGATCTTGTTTAAAAACATTAAACAGATTCTGTCAVKCTTTMAAAAAAAGCCATGA
 3364
 AATTNTAGCAAGCCACTGAATTGAGTTTTCACCTTTGGTTTCTAATAATGCTGTGTAATCAGANCAGKTTTCTTACCCCT
 3443
 TTCTTGGTCTTAAATTTCCCTTACTGATAAAAATGGGGTWTAAATACCTATCTCAAAAAATTATTGCACATATTARATAACA
 3522
 TTCCTCTATGTATCTCAATGGCATTAGACATTAGGAGAAGCATTTTGTGGAGGATTTGAAGTTGAGATCTTCATCCAAG
 3601
 AAGTAGCTTTTCAATTTGSTAGAAGCTTAATGTAGGCAAGCCACTTCATTTTTCAGAACTTGTTTACTCATTTATAATA
 3680
 TGGGAATAAAAAATTTGTGCAAGTCAGAGAAAGGTGCCCTTAAAAATGTTGTGGCCCAAGCCACATGAGATCAAAGACACAC
 3759
 TTTTTCATGACCTCAAATGTGGGCCCCAGCCTAGGTCAGCCAAACCCCATCCAAACCTTAGACTCACGAACAAATCCACCT
 3838
 GAGATCAGCAGAGCCACCCTAGATCAGCTGAAACTCTAAGCACAAAATAAAAACTTATCACTGTAAAAAATAAAAAA
 3917
 AAAAAAA
 3925

Fig. 11S

GAGACTGTGAAGAAGGAACGTTGCTTGGGCAAAAGGAGCATATTTCTCAGGAGACGGGGCCCTGCCTGCCACACCA	79
AGCATTAGGCCACCAGGAAGACCCCCCATCTGCAAGCAAGCCTAGCCTTCCAGGGAGAAAGAGGCCCTGCAGCTCCTTC	158
M N W H M I I S G L I V V L K V V G	19
ATC ATG AAC TGG CAC ATG ATC ATC TCT GGG CTT ATT GTG GTA GTG CTT AAA GTT GTT GGA	218
M T L F L L Y F C P K D W E F Y Q A R C	39
ATG ACC TTA TTT CTA CTT TAT TTC TGC CCC AAA GAC TGG GAA TTT TAT CAA GCA AGA TGT	278
F F L S T S E S S W N E S R D F C K G K	59
TTT TTC TTA TCC ACT TCT GAA TCA TCT TGG AAT GAA AGC AGG GAC TTT TGC AAA GGA AAA	338
G S T L A I V N T P E K L K F L Q D I T	79
GGA TCC ACA TTG GCA ATT GTC AAC ACG CCA GAG AAA CTG AAG TTT CTT CAG GAC ATA ACT	398
D A E K Y F I G L I Y H R E E K R W R W	99
GAT GCT GAG AAG TAT TTT ATT GGC TTA ATT TAC CAT CGT GAA GAG AAA AGG TGG CGT TGG	458
I N N S V F N G K Y V N M P Q F P G D L	119
ATC AAC AAC TCT GTG TTC AAT GGC AAG TAC GTG AAC ATG CCA CAG TTT CCT GGG GAT CTT	518
G L L Q K T K P E I A G F T L E *	135
GGT TTG CTT CAA AAG ACC AAA CCT GAG ATT GCT GGG TTC ACC CTG GAA TAG	569

Fig. 11T

CTCAAACGCTGACACTTGACTCTGTGTTCTGCTCTTCTCTCCCTTTCTTCCAACCCATCTATTCCCTATCTGTCTACCAGTAGC 648
 GGTCCCTTGCCCCATTGGGAAACTGAGCTTCTTTCTTCTGCACTGGGGACTGGATGCTAGCCATCTCCAGGAGACAGGA 727
 TCAGTTTTACGGAAACAACCTCAGTTAGTATAGAGATGAGGTCCGCTTCTGTAGTACTGAGCAATTTCTGACTGATCAAAA 806
 AGCCCTAGTCTGTTGACAGGGTTTGTATTTTATTTTAGCCCTCAGAGTATACCATACTAGGTCCCTGTGACTTCGTCTCTGTTCTCAA 885
 AAATTATAAAACATTTATTAGGGATTACCATGGTGGAAAGAGGGATAAACATAGGTCCCTGTGACTTCGTCTCTGTTCTCA 964
 GGGAAACCCCATTCACATGCCCCCTCCTAACCTCCAAGCGAGGGTAGCAGAGGCTCTCCCTCAGTCTGAACCTAAGGCTTGG 1043
 CCTTGGGAGGGCTCCTAGTCTGAGCTTGGAGCAGCACGGACAGCAATGTTTATGGGAATGGAGAGAGGCTCTGGG 1122
 CAGGATAGGAAACCTTCTTGGAGACCCCTTTGAAGAAAACCAGGCAGCCAAAGGAGCCAAACACACTAGATTTCGTGTTCT 1201
 TCAGCAAAGCCCTGAAGAGACACTTAAGCTAAAAATTCCTTGTCTATATTTCTGAAACTCCCATTTAACAATATGTAACCT 1280
 CCTTTGTAAACCAAAATTTAGGTAAGCAGGCTTCCCTTGTCTCTGAAGGTTTGTAGTACCTGGCTGTATTTTGTGTGAGTATT 1359
 TTTAAAAATTTTGGATAGTCTCTTAGGCAACAATAATCAACAATATATTTCATCCCTTCAGTTCTGGAGAAAAGCCTGATACC 1438
 AGGCACAGCCTACTGACCCCAAGGAGCCTGGCACTGATTGGCATCACATTTGATCTAGAACTGGTCCAGCCGCCGAAGAG 1517
 TAGGAAAAGAGAAAGGCTGCTCAGGGAAAACATTTGGCTGGGGCACGGAATAAGCACATAGTAAAAAGGGAACATCAGGG 1596
 TCAAAATGGAAATCACCTGAGACAGGAAACAGGGAGTTTCATTTTGGCCACACTGGAGAAAGCAAGAGAAAGAGAACACAA 1675
 GTCTTGGAGTACCCCTGGCTGTTCTCCACACTCAACAAGACATCAGCTATATACTCTGCTTGGTGCATAAGAAAAGAGAAAAGA 1754
 GATGCCCTTTTGTGTTTGTAGTAAGAAATAATTAAACCATAGGAAGACCATGTATAAAACTGATGGAATAATAGTCACC 1833
 AAAGTACAGCACATACCAATTTGTGTCATAATAACAATGTAGCACAGTAATGACTGTACATGTTCATTTGTATGTATACCAA 1912
 ACAAGATTGTTGTAAATCATATTTTATTTTATTAACAACATAAGTTCTGTCTTCTGCAATTCCTAGGTTTCATCATTTTGGCT 1991
 CCTTAGCATGGCCACTTACAATTTTAAACATGAGATAACACATCAGGTGTCAGAACTTGCTTGAAGGGAATTACCAGA 2070
 AGTAATTTGTGTTTGAGATGGGTGGAATTTGGAATTTATATTAGTAGCCGGTGGAGATACAAAGTTCTCTGACTGTGTTG 2149
 GGAAAGGATAAGTGCTACCGTTGAGAAAGGAAGAGCTGAGTCTAGGTGGAGAAAAATATCAACAGAACTCTAGCCA 2228
 AAGGCAAGCCCCAGAACTCAGACAAACAGAAAGGAAATCCTAATCCTTCTGTTTGTAGAGAGAGAACTGTAGTTGCTTC 2307
 ACTTCCCTATTTCATGACAGAATAACTGCAAACTTTTAAAGATCAGGAAATGTAGACATCTAGTGATTCTCTTTAGTAGACA 2386

Fig. 11U

GTTTAATTCCCCAAGATTAGGAGACACTTCTGTGCAGGTTCTAAAGGAGCCCCAATGGCCTGGGGTGGGAGTGGGGA 2465
 GTAGATAGGGAATATGTGGGATTTGGTTTAAGTTCATCATTTGGGAGAGTTCTCTGGATCCTTGCAAGCTTAGATATAATGT 2544
 GATCTTTATTAGATAGCAGTGGCATGCTTTTAAAAAAGGCAATGAAAATTTAGCAAGCCACTGAATTTGAGTTTT 2623
 CACTTTGTTTCTAATATGCTGTGTGAATCAGTACAGTTTCTTACCCTTTCTTGGTCTTAATTTCCCTTACTGATAAAAT 2702
 GGGGTAGTAATACCTATCTCAAAAAATTATTGCACATATTAAATAACATTCCTCTATGTATCTCAATGGCATTAGACAT 2781
 TAGGAGAAGCATTTTGTGGAGGATTTTGAAGTTGAGATCTTTCATCCAAAGAGTAGCTTTTCAATTTGCTAGAAAGCTTAAT 2860
 GTAGGCAAGCCACTTCAATTTTCAGAACTTGTTTTACTCATTTATAATATGGGAATAAAAAATTTGTGCAAGTCAGAGAAG 2939
 GGTGCCCTTAAAAATGTTGTGCCAAGCCACATGAGATCAAGACACACACTTTTCATGACCTCAAATGTGGGCCCAGCCTA 3018
 GGTAGCCAAACCCCATCCAAACCTTAGACTCAGCAACAAATCCACCTGAGATCAGCAGAGCCACCCTAGATCAGCTGA 3097
 AACTCTAAGCACAAAAATAAAAACTTATCAGTGTAAAAAAGTCTCTCGTATAGCAAAATCTAA 3176
 CTGATGCAATCTCCATCTGGCCCTTCATCCCTTATTTGTCCTTTTCGTGTAATTGTTTCATCCAGCAACCAGGATGA 3255
 TCTTGTAAAAACATTAACAGATTCTGTCAVKCTTTMAAAAAAAGCCCATGAAATTTNTAGCAAGCCACTGAAATTT 3334
 GAGTTTTCACCTTTGTTTCTAATATGCTGTGTGAATCAGANCAGKTTTCTTACCTTTTCTTGGTCTTAATTTCCCTTACT 3413
 GATAAAATGGGGTGTAAATACCTATCTCAAAAAATTATTGCACATATTARATAACATTCCTCTATGTATCTCAATGGCA 3492
 TTAGACATTAGGAGAAGCATTTTGTGGAGGATTTGAAGTTGAGATCTTCATCCAAAGAGTAGCTTTTCAATTTGSTAGA 3571
 AGCTTAATGTAGGCAAGCCACTTCAATTTTCAGAACTTGTTTTACTCATTTATAATATGGGAATAAAAAATTTGTGCAAGT 3650
 CAGAGAAGGGTGCCCTTAAAAATGTTGTGGCCCAAGCCACATGAGATCAAGACACACACTTTTCATGACCTCAAATGTGGGC 3729
 CCAGCCTAGGTCAGCCAAACCCCATCCAAACCTTAGACTCACGAACAAATCCACCTGAGATCAGCAGAGCCACCCCTAGA 3808
 TCAGCTGAAAACCTTAAGCACAAAAATAAAAACTTATCACTGTAAAAAAGTAAAAAAGAAAGCAACCTGCCCCG 3887
 GCGGGCCGCC 3898

Fig. 11V

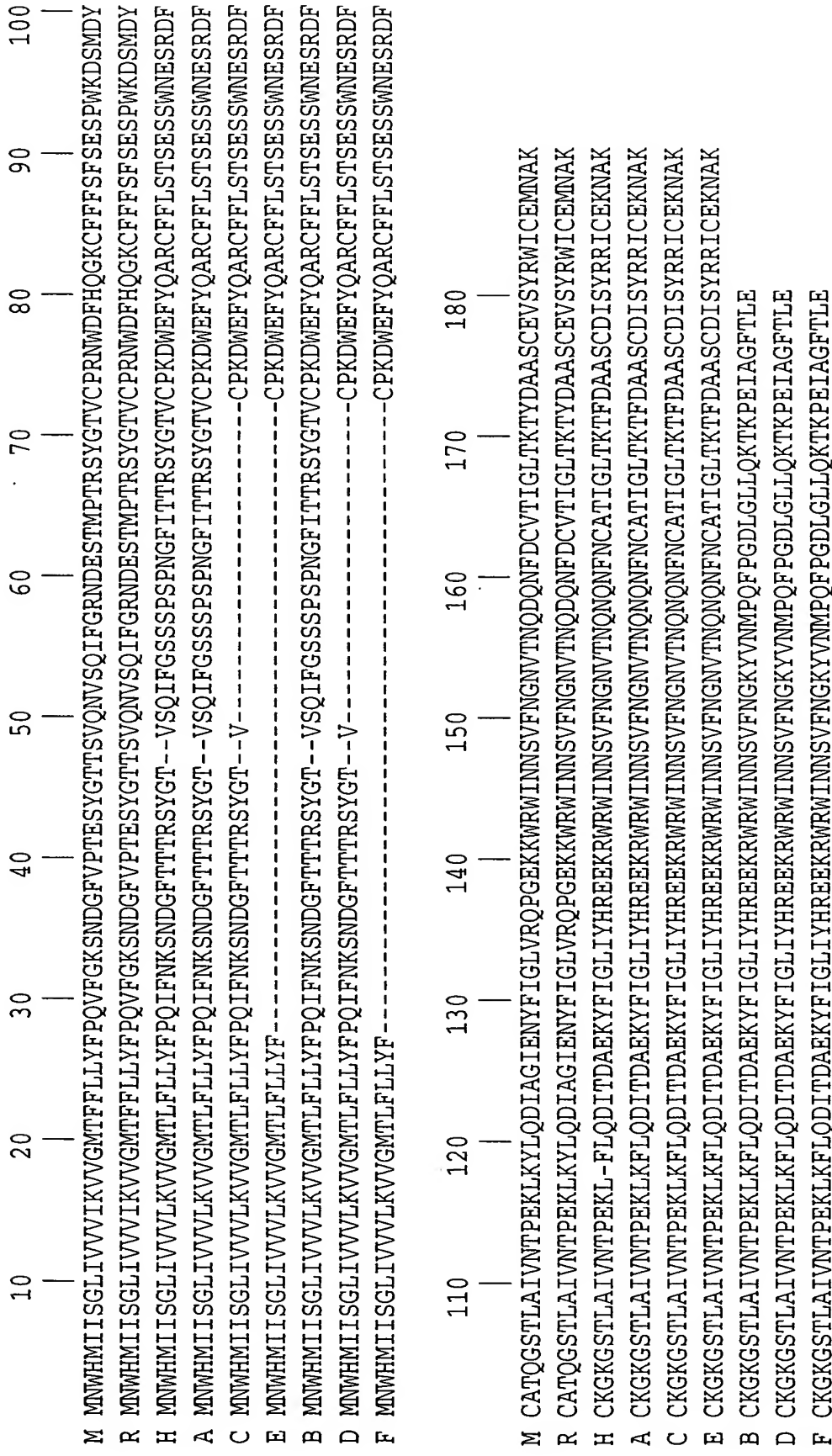


Fig. 11W

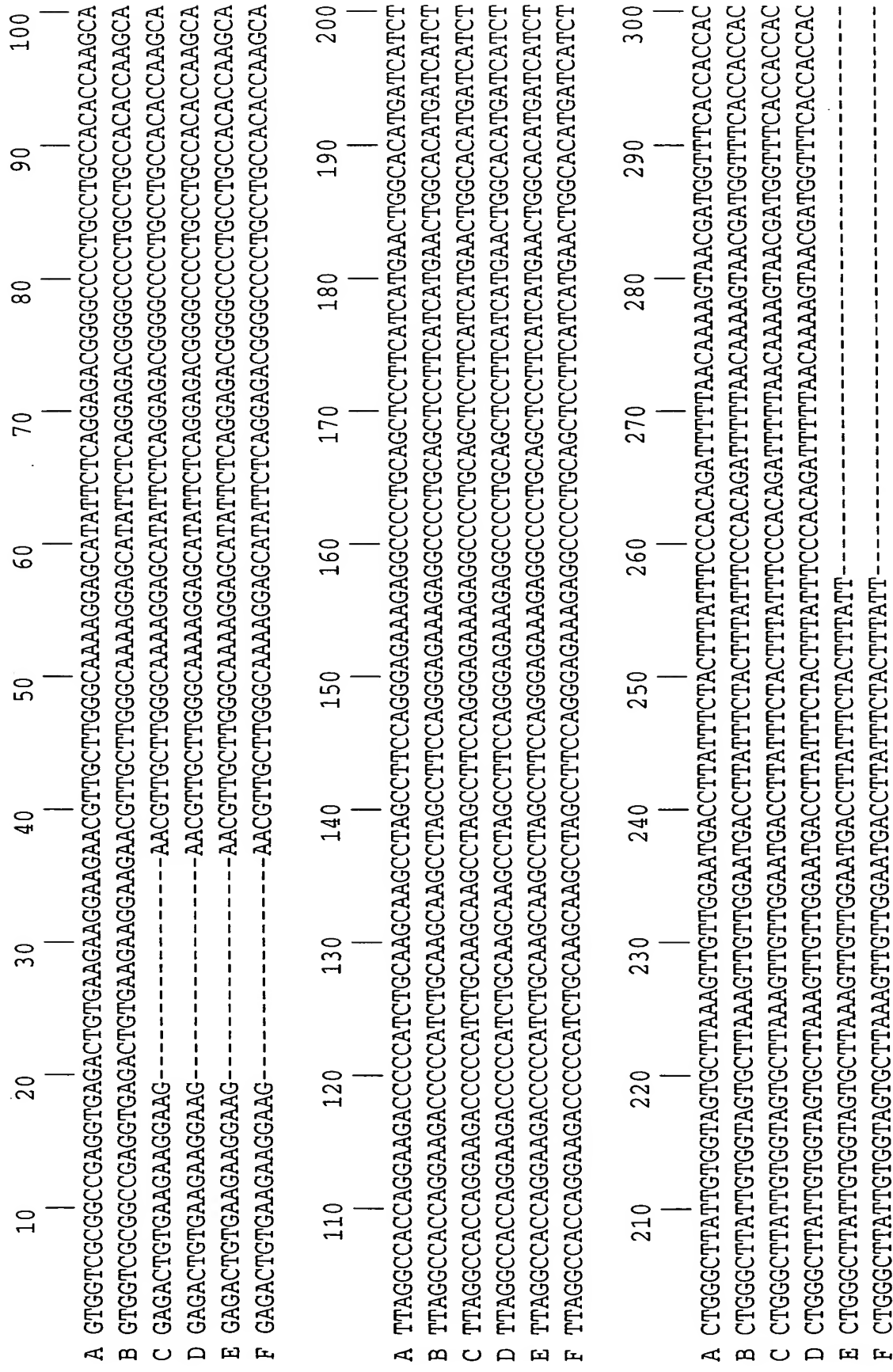


Fig. 11X-1

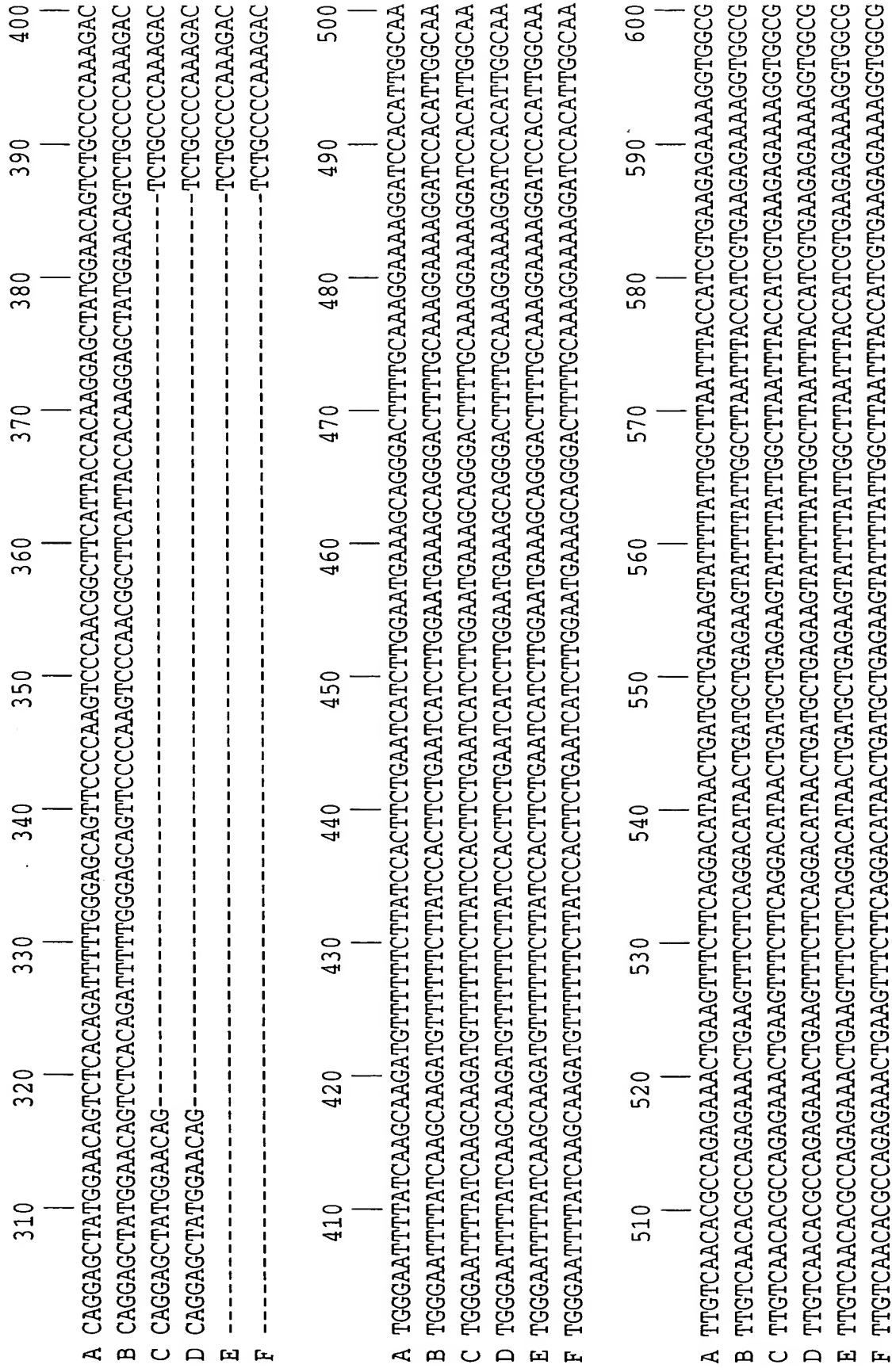


Fig. 11X-2

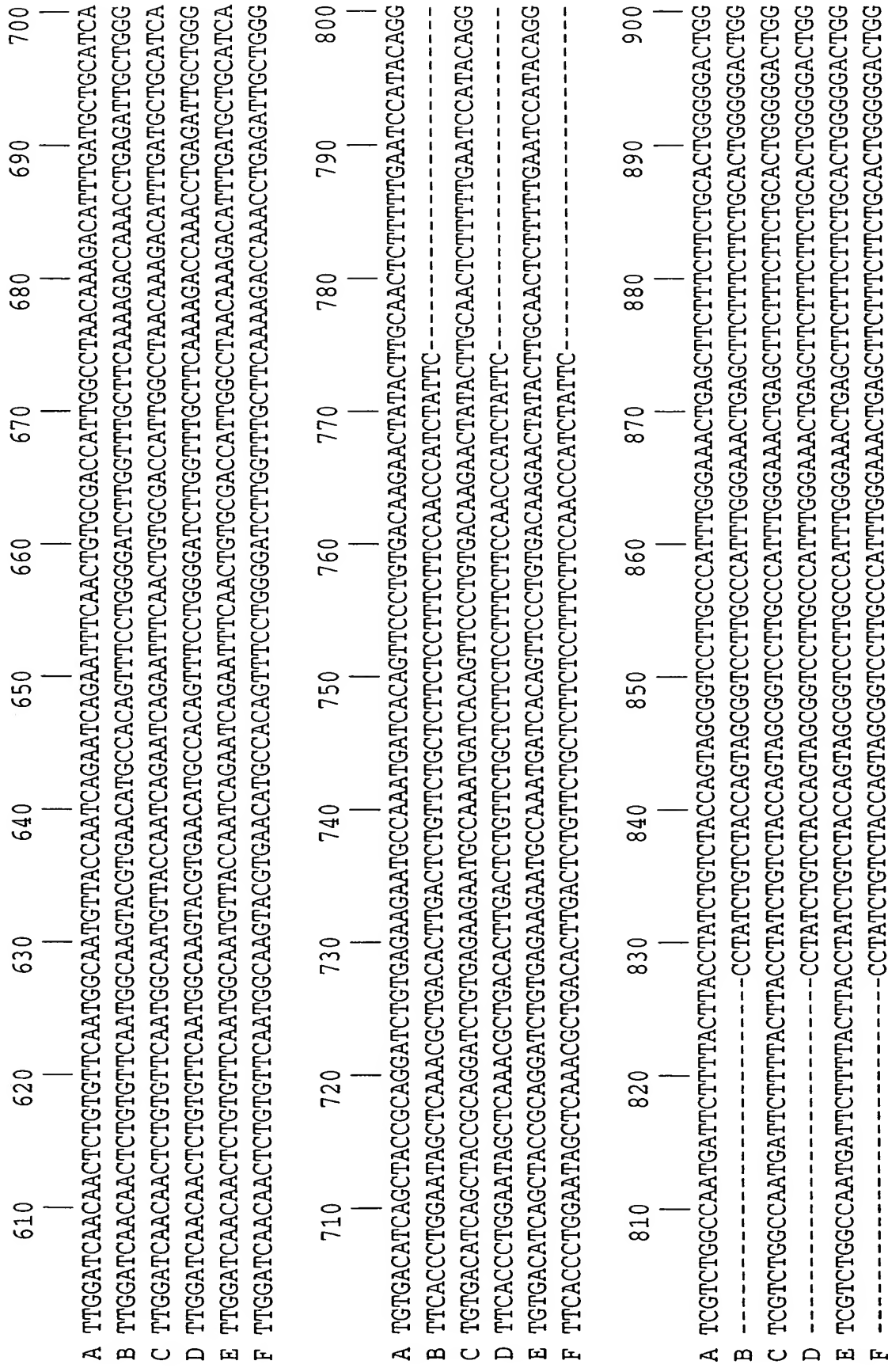


Fig. 11X-3

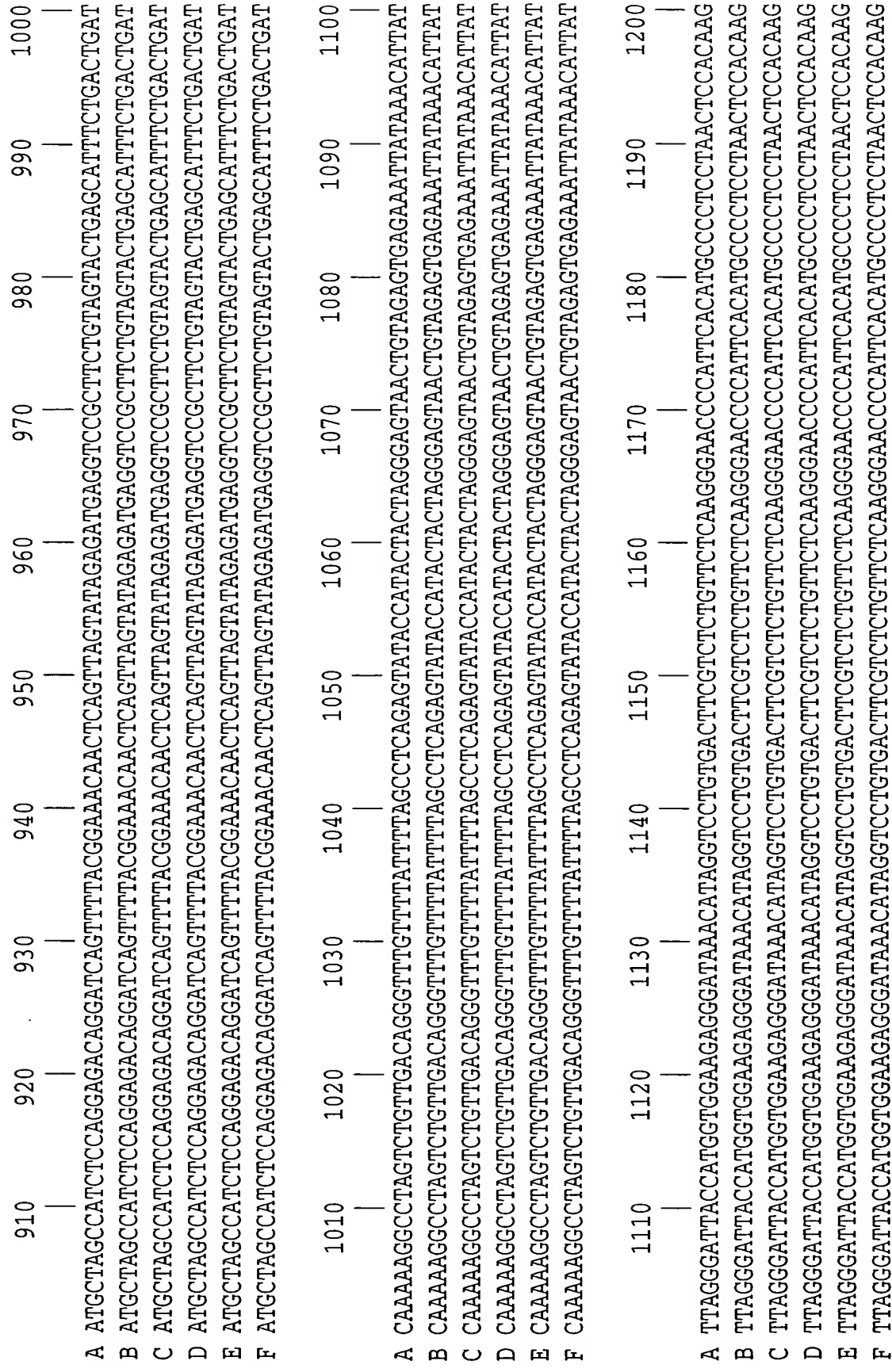


Fig. 11X-4

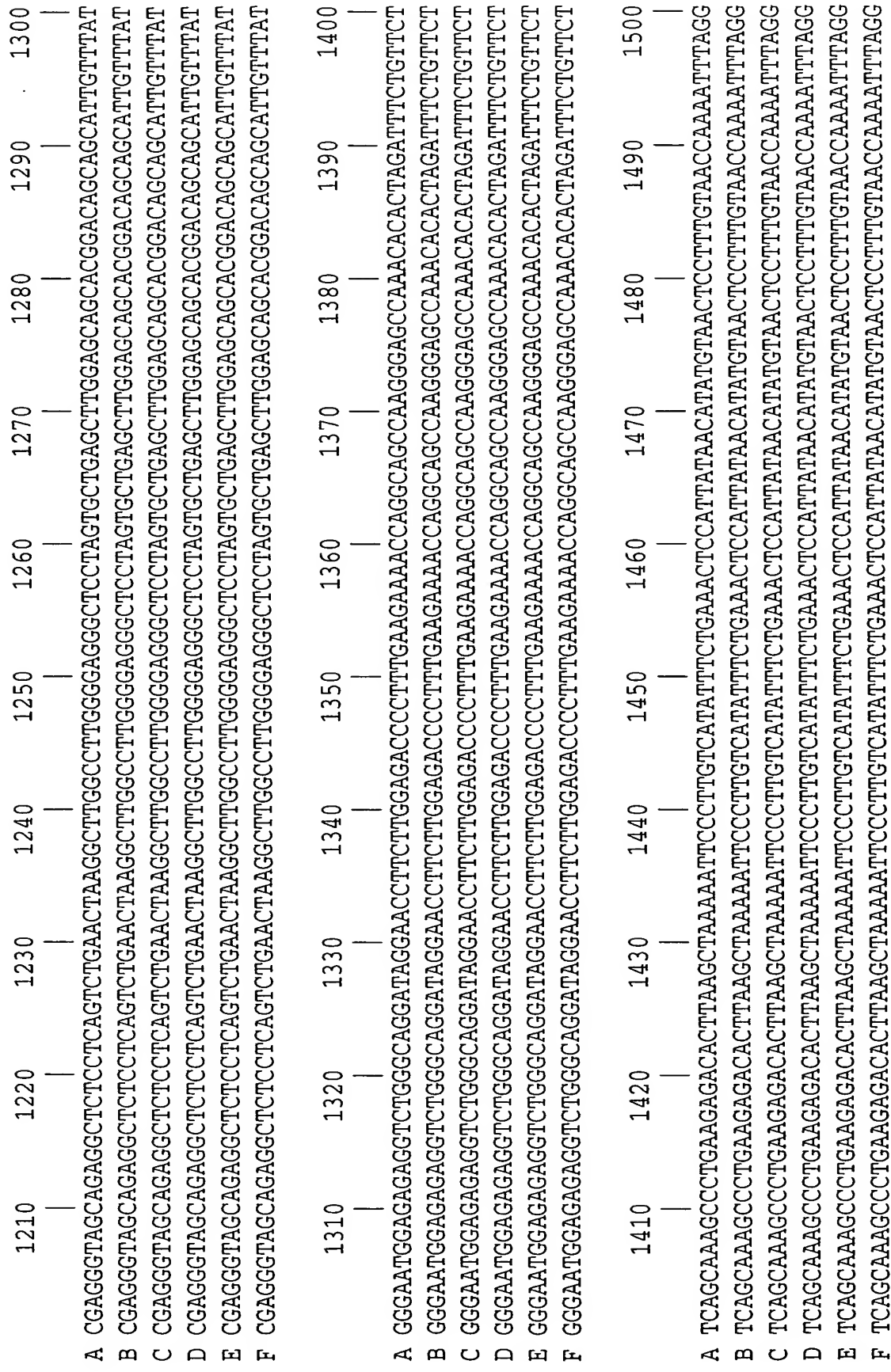


Fig. 11X-5

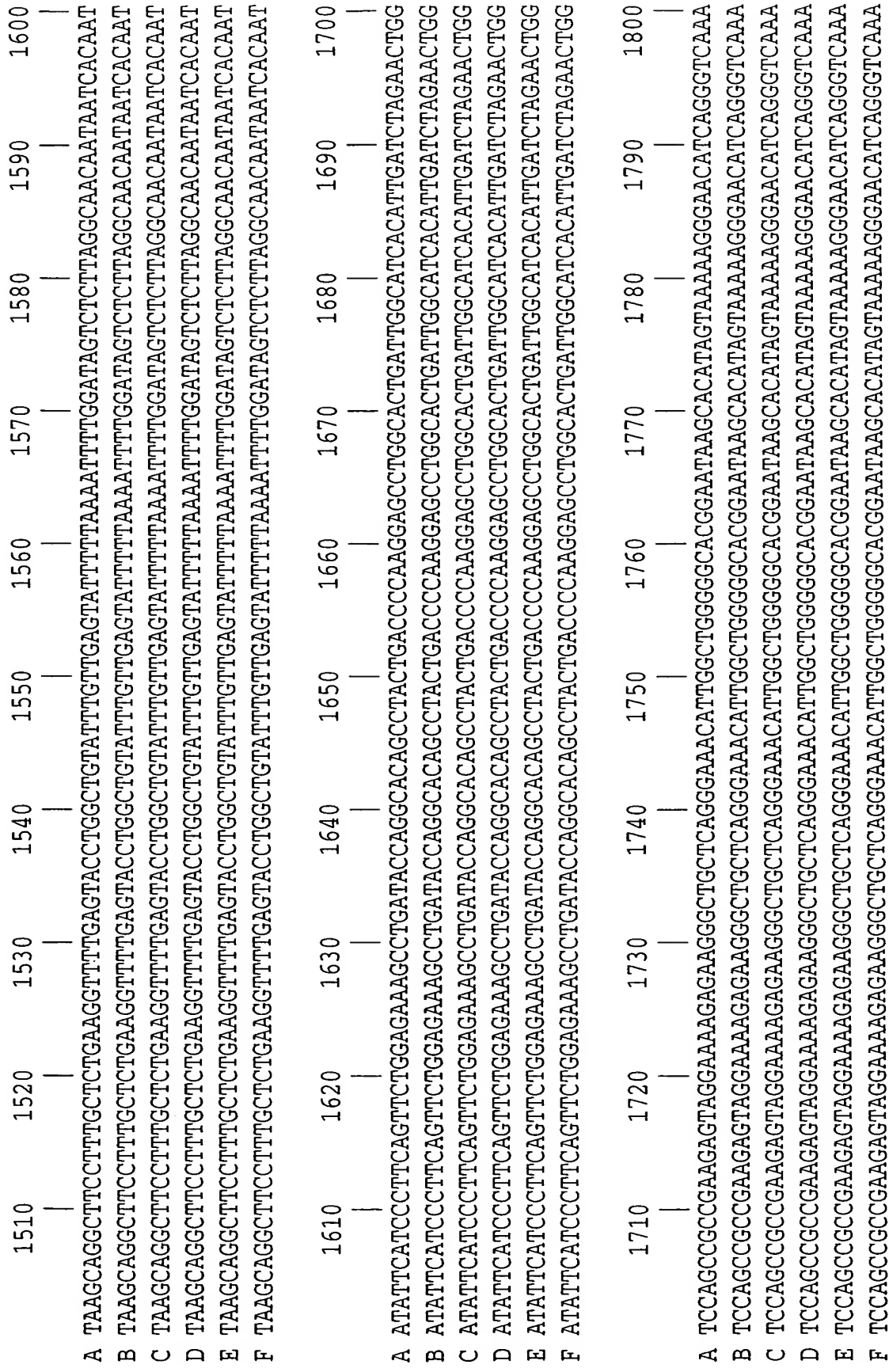


Fig. 11X-6

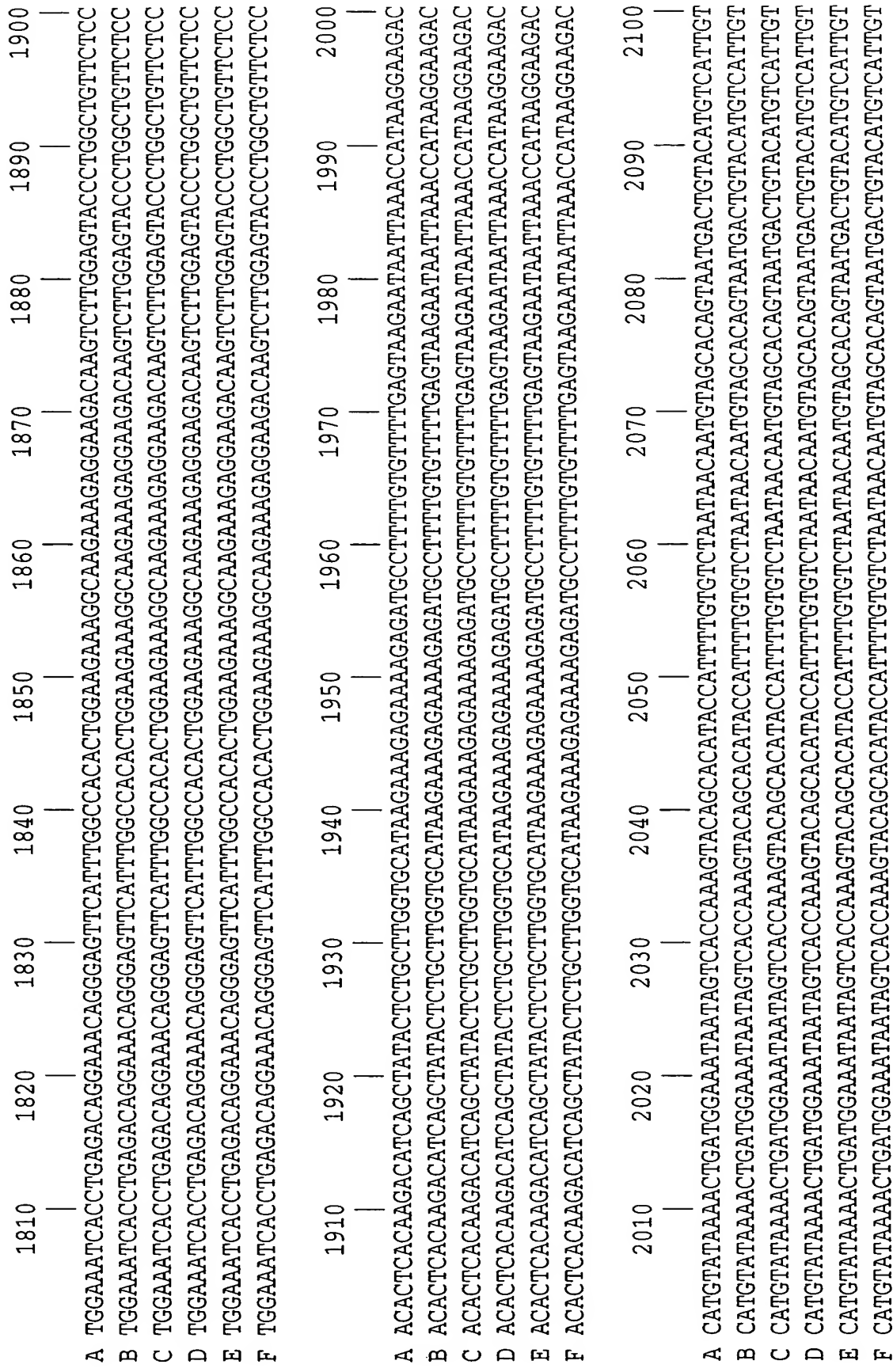


Fig. 11X-7

	2110	2120	2130	2140	2150	2160	2170	2180	2190	2200
A	ATGTATACCAAA	CAAGATTGTT	GTAAATCAT	ATATTTTAT	TACAACACT	AAAGTTCT	GTCTCTGC	ATTCCCTAG	GTTCATCAT	TTTTTGGCTCCCTTAGCATG
B	ATGTATACCAAA	CAAGATTGTT	GTAAATCAT	ATATTTTAT	TACAACACT	AAAGTTCT	GTCTCTGC	ATTCCCTAG	GTTCATCAT	TTTTTGGCTCCCTTAGCATG
C	ATGTATACCAAA	CAAGATTGTT	GTAAATCAT	ATATTTTAT	TACAACACT	AAAGTTCT	GTCTCTGC	ATTCCCTAG	GTTCATCAT	TTTTTGGCTCCCTTAGCATG
D	ATGTATACCAAA	CAAGATTGTT	GTAAATCAT	ATATTTTAT	TACAACACT	AAAGTTCT	GTCTCTGC	ATTCCCTAG	GTTCATCAT	TTTTTGGCTCCCTTAGCATG
E	ATGTATACCAAA	CAAGATTGTT	GTAAATCAT	ATATTTTAT	TACAACACT	AAAGTTCT	GTCTCTGC	ATTCCCTAG	GTTCATCAT	TTTTTGGCTCCCTTAGCATG
F	ATGTATACCAAA	CAAGATTGTT	GTAAATCAT	ATATTTTAT	TACAACACT	AAAGTTCT	GTCTCTGC	ATTCCCTAG	GTTCATCAT	TTTTTGGCTCCCTTAGCATG
	2210	2220	2230	2240	2250	2260	2270	2280	2290	2300
A	GCCACTTACAA	ATTTTAA	CATGAGATA	AAACACAT	CAGGTGTC	CAGAACTT	GCCTTGA	AGGGAATT	ACCAGAA	GTAAATTTGTGTTGAGATGGGGTGGAAATT
B	GCCACTTACAA	ATTTTAA	CATGAGATA	AAACACAT	CAGGTGTC	CAGAACTT	GCCTTGA	AGGGAATT	ACCAGAA	GTAAATTTGTGTTGAGATGGGGTGGAAATT
C	GCCACTTACAA	ATTTTAA	CATGAGATA	AAACACAT	CAGGTGTC	CAGAACTT	GCCTTGA	AGGGAATT	ACCAGAA	GTAAATTTGTGTTGAGATGGGGTGGAAATT
D	GCCACTTACAA	ATTTTAA	CATGAGATA	AAACACAT	CAGGTGTC	CAGAACTT	GCCTTGA	AGGGAATT	ACCAGAA	GTAAATTTGTGTTGAGATGGGGTGGAAATT
E	GCCACTTACAA	ATTTTAA	CATGAGATA	AAACACAT	CAGGTGTC	CAGAACTT	GCCTTGA	AGGGAATT	ACCAGAA	GTAAATTTGTGTTGAGATGGGGTGGAAATT
F	GCCACTTACAA	ATTTTAA	CATGAGATA	AAACACAT	CAGGTGTC	CAGAACTT	GCCTTGA	AGGGAATT	ACCAGAA	GTAAATTTGTGTTGAGATGGGGTGGAAATT
	2310	2320	2330	2340	2350	2360	2370	2380	2390	2400
A	GGAATTATAT	AGTAGCCGGT	GGAGATACA	AGTTCTCT	GACTGTCT	GAGTAA	AGGATAAG	TGCTAC	CGTTGAGA	AGGGAAGAAAGGCTGAGTCTAGGTGG
B	GGAATTATAT	AGTAGCCGGT	GGAGATACA	AGTTCTCT	GACTGTCT	GAGTAA	AGGATAAG	TGCTAC	CGTTGAGA	AGGGAAGAAAGGCTGAGTCTAGGTGG
C	GGAATTATAT	AGTAGCCGGT	GGAGATACA	AGTTCTCT	GACTGTCT	GAGTAA	AGGATAAG	TGCTAC	CGTTGAGA	AGGGAAGAAAGGCTGAGTCTAGGTGG
D	GGAATTATAT	AGTAGCCGGT	GGAGATACA	AGTTCTCT	GACTGTCT	GAGTAA	AGGATAAG	TGCTAC	CGTTGAGA	AGGGAAGAAAGGCTGAGTCTAGGTGG
E	GGAATTATAT	AGTAGCCGGT	GGAGATACA	AGTTCTCT	GACTGTCT	GAGTAA	AGGATAAG	TGCTAC	CGTTGAGA	AGGGAAGAAAGGCTGAGTCTAGGTGG
F	GGAATTATAT	AGTAGCCGGT	GGAGATACA	AGTTCTCT	GACTGTCT	GAGTAA	AGGATAAG	TGCTAC	CGTTGAGA	AGGGAAGAAAGGCTGAGTCTAGGTGG

Fig. 11X-8

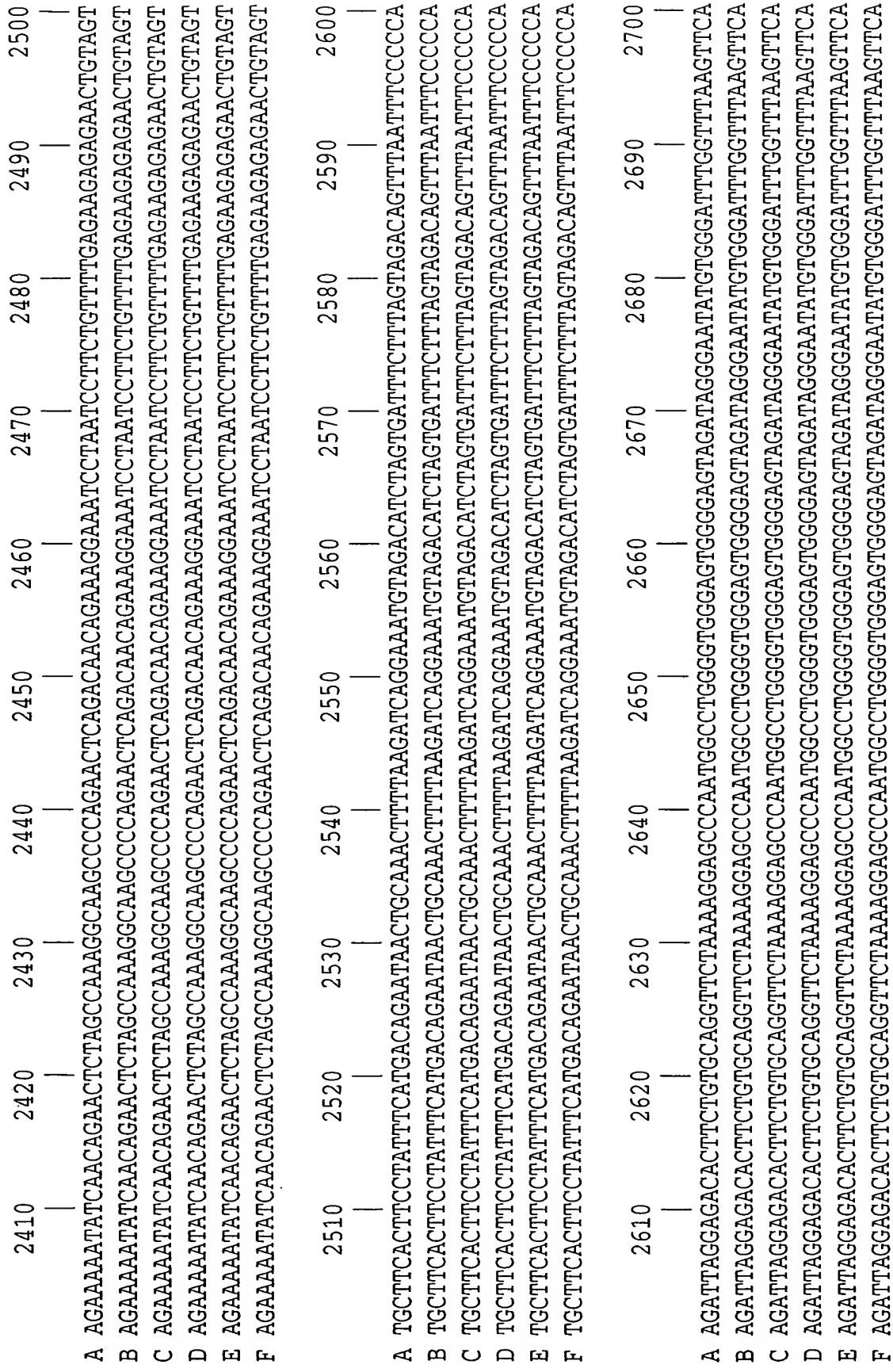


Fig. 11X-9

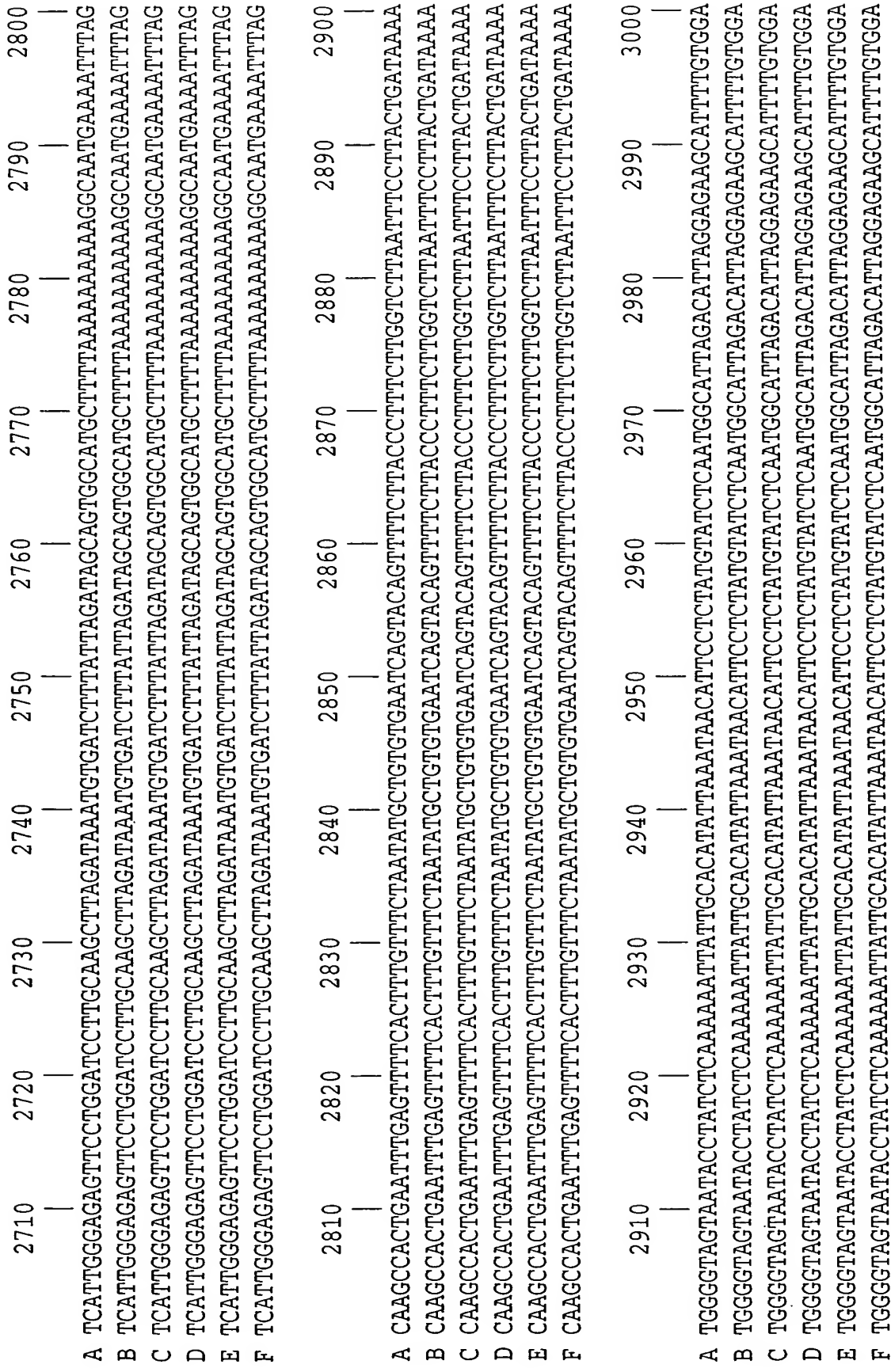


Fig. 11X-10

	3010	3020	3030	3040	3050	3060	3070	3080	3090	3100
A	GGATTTGAAGTTGAGATCTTTCATCCAAAGAAAGTAGCTTTTCAATTGCTAGAAGCTTAATGTAGCCAAGCCACTTCATTTTTCAGAACTTGTTTACTCATTT									
B	GGATTTGAAGTTGAGATCTTTCATCCAAAGAAAGTAGCTTTTCAATTGCTAGAAGCTTAATGTAGCCAAGCCACTTCATTTTTCAGAACTTGTTTACTCATTT									
C	GGATTTGAAGTTGAGATCTTTCATCCAAAGAAAGTAGCTTTTCAATTGCTAGAAGCTTAATGTAGCCAAGCCACTTCATTTTTCAGAACTTGTTTACTCATTT									
D	GGATTTGAAGTTGAGATCTTTCATCCAAAGAAAGTAGCTTTTCAATTGCTAGAAGCTTAATGTAGCCAAGCCACTTCATTTTTCAGAACTTGTTTACTCATTT									
E	GGATTTGAAGTTGAGATCTTTCATCCAAAGAAAGTAGCTTTTCAATTGCTAGAAGCTTAATGTAGCCAAGCCACTTCATTTTTCAGAACTTGTTTACTCATTT									
F	GGATTTGAAGTTGAGATCTTTCATCCAAAGAAAGTAGCTTTTCAATTGCTAGAAGCTTAATGTAGCCAAGCCACTTCATTTTTCAGAACTTGTTTACTCATTT									
	3110	3120	3130	3140	3150	3160	3170	3180	3190	3200
A	TATAAATATGGGAATAAAAAATTTGTGCAAGTCAGAGAAGGGTGCCCTTAAAAAATGTTGTGGCCAAAGCCACATGAGATCAAAGACACACACTTTTTCATGACCTCA									
B	TATAAATATGGGAATAAAAAATTTGTGCAAGTCAGAGAAGGGTGCCCTTAAAAAATGTTGTGGCCAAAGCCACATGAGATCAAAGACACACACTTTTTCATGACCTCA									
C	TATAAATATGGGAATAAAAAATTTGTGCAAGTCAGAGAAGGGTGCCCTTAAAAAATGTTGTGGCCAAAGCCACATGAGATCAAAGACACACACTTTTTCATGACCTCA									
D	TATAAATATGGGAATAAAAAATTTGTGCAAGTCAGAGAAGGGTGCCCTTAAAAAATGTTGTGGCCAAAGCCACATGAGATCAAAGACACACACTTTTTCATGACCTCA									
E	TATAAATATGGGAATAAAAAATTTGTGCAAGTCAGAGAAGGGTGCCCTTAAAAAATGTTGTGGCCAAAGCCACATGAGATCAAAGACACACACTTTTTCATGACCTCA									
F	TATAAATATGGGAATAAAAAATTTGTGCAAGTCAGAGAAGGGTGCCCTTAAAAAATGTTGTGGCCAAAGCCACATGAGATCAAAGACACACACTTTTTCATGACCTCA									
	3210	3220	3230	3240	3250	3260	3270	3280	3290	3300
A	AATGTGGGCCCAGCCTAGGTCAGCCAAACCCCCATCCAAACCCCTTAGACTCACGAACAAATCCACCTGAGATCAGCAGAGCCACCCCTAGATCAGCTGAAACT									
B	AATGTGGGCCCAGCCTAGGTCAGCCAAACCCCCATCCAAACCCCTTAGACTCACGAACAAATCCACCTGAGATCAGCAGAGCCACCCCTAGATCAGCTGAAACT									
C	AATGTGGGCCCAGCCTAGGTCAGCCAAACCCCCATCCAAACCCCTTAGACTCACGAACAAATCCACCTGAGATCAGCAGAGCCACCCCTAGATCAGCTGAAACT									
D	AATGTGGGCCCAGCCTAGGTCAGCCAAACCCCCATCCAAACCCCTTAGACTCACGAACAAATCCACCTGAGATCAGCAGAGCCACCCCTAGATCAGCTGAAACT									
E	AATGTGGGCCCAGCCTAGGTCAGCCAAACCCCCATCCAAACCCCTTAGACTCACGAACAAATCCACCTGAGATCAGCAGAGCCACCCCTAGATCAGCTGAAACT									
F	AATGTGGGCCCAGCCTAGGTCAGCCAAACCCCCATCCAAACCCCTTAGACTCACGAACAAATCCACCTGAGATCAGCAGAGCCACCCCTAGATCAGCTGAAACT									

Fig. 11X-11

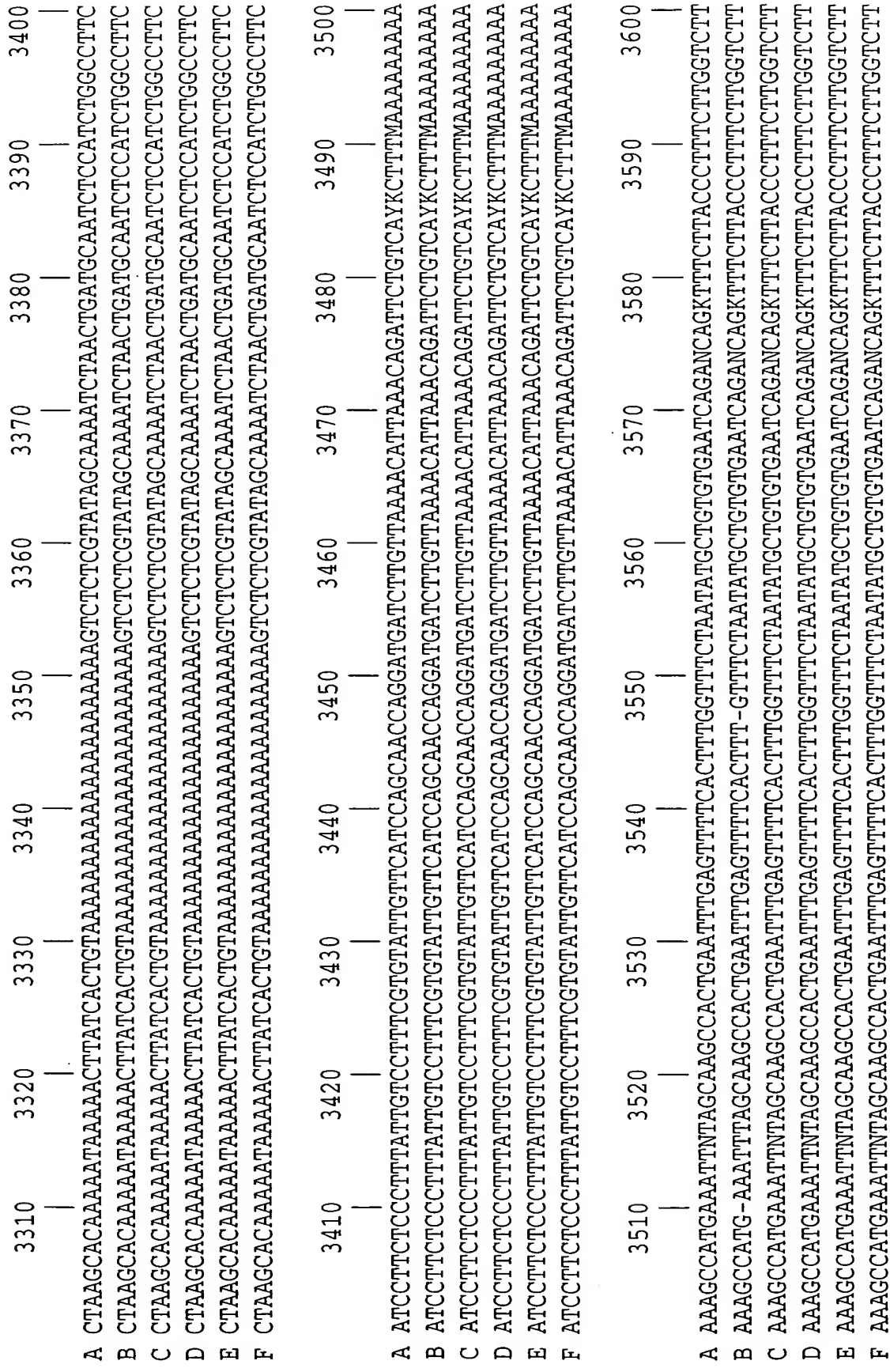


Fig. 11X-12

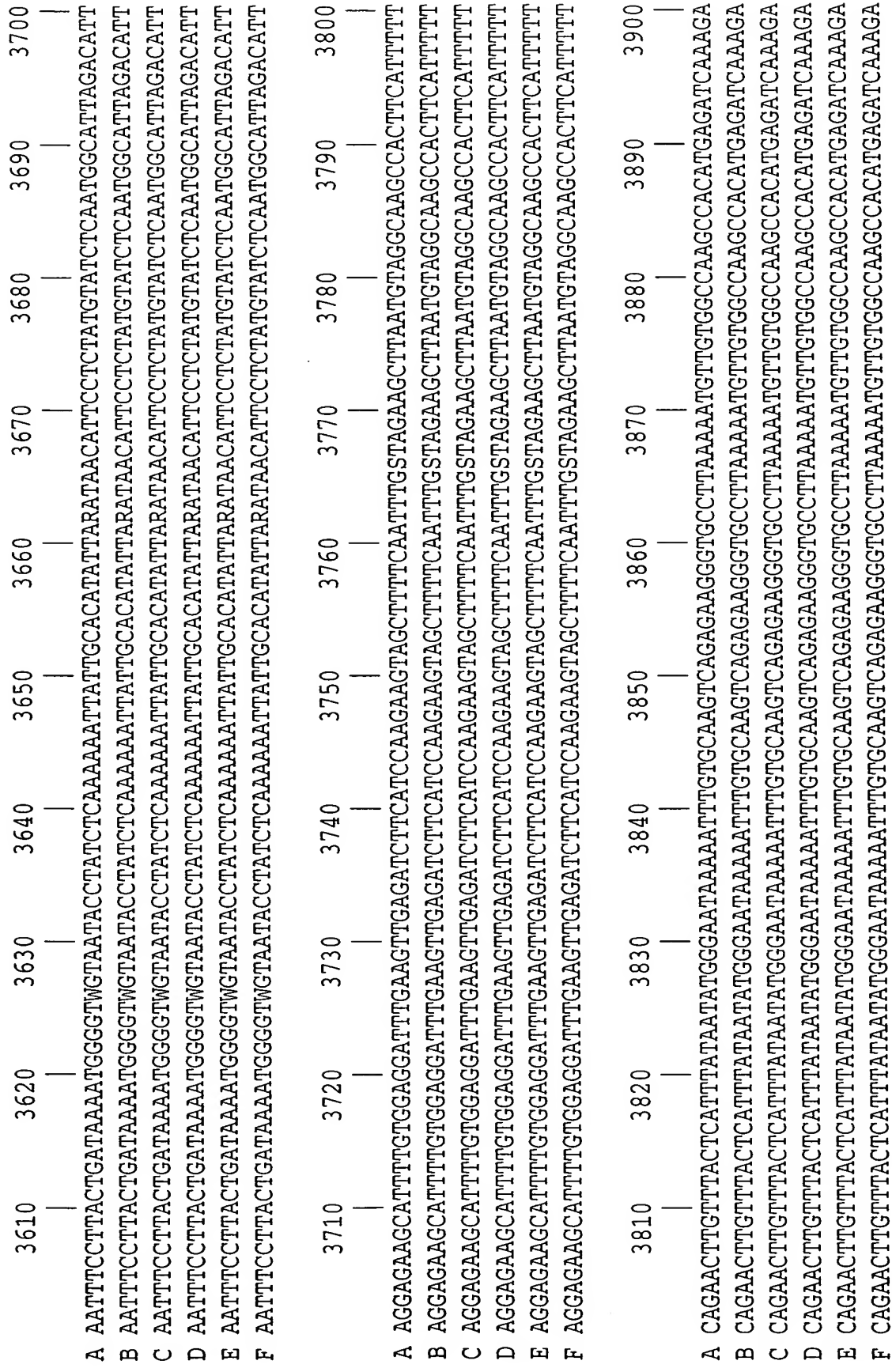


Fig. 11X-13

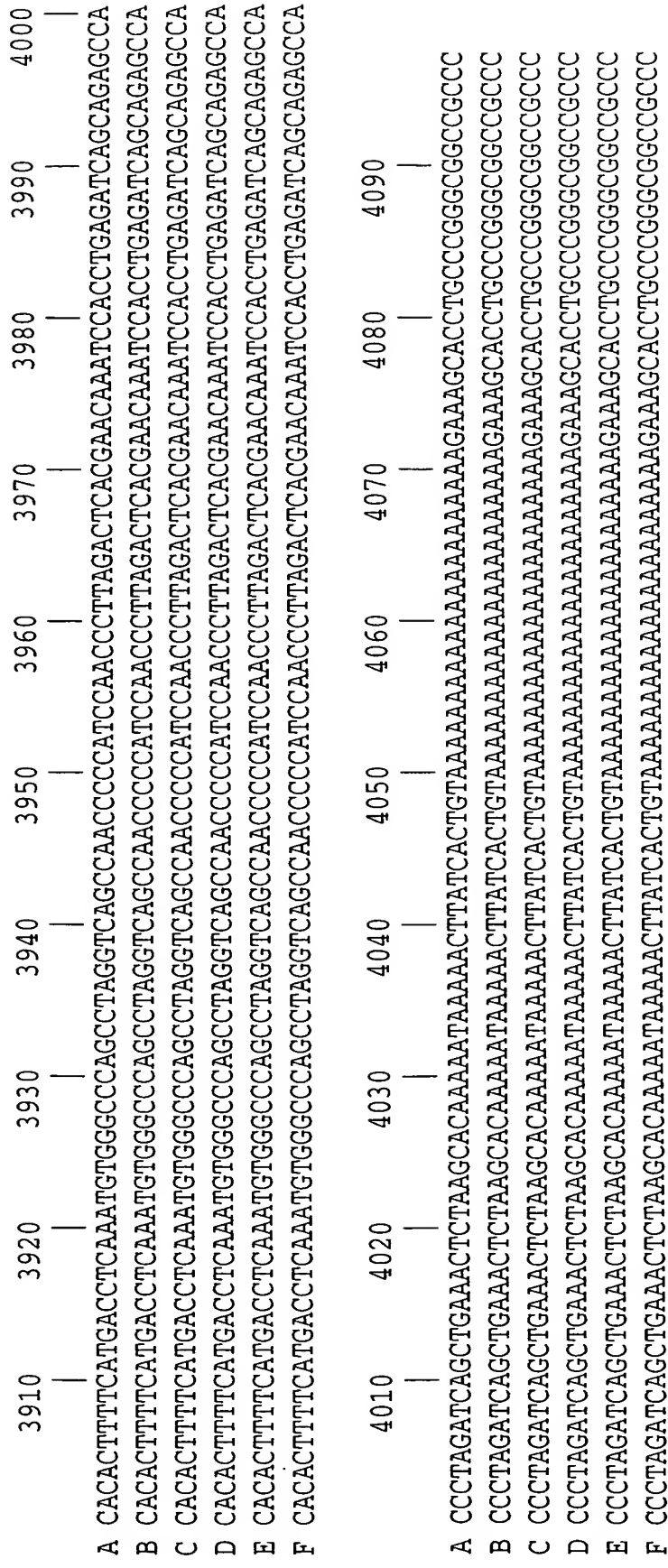


Fig. 11X-14

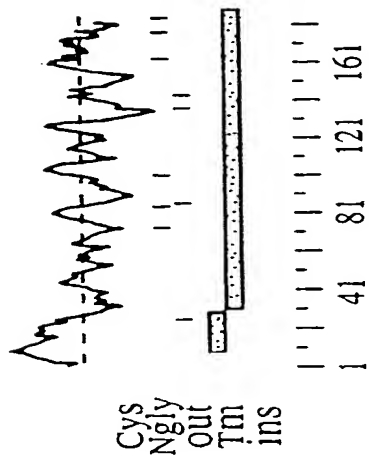


Fig. 11Y-1

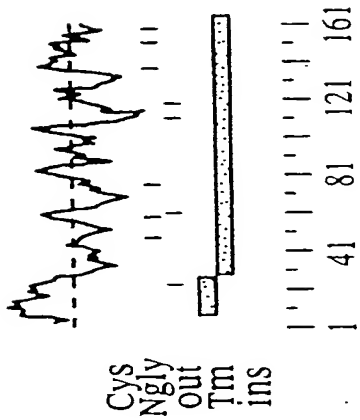


Fig. 11Y-3

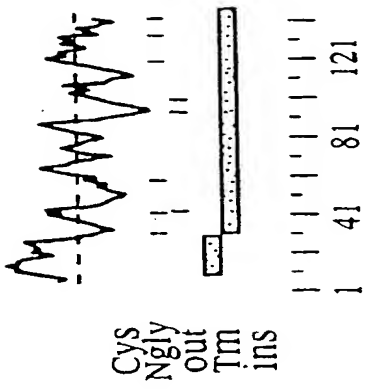


Fig. 11Y-5

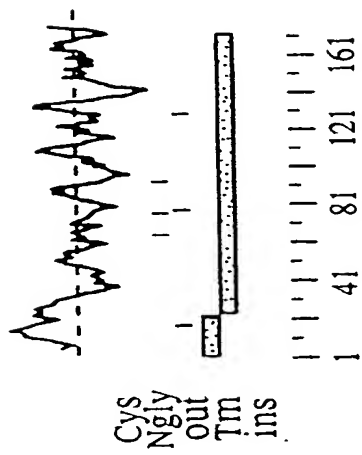


Fig. 11Y-2

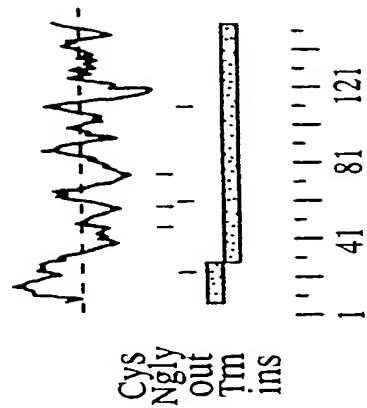


Fig. 11Y-4

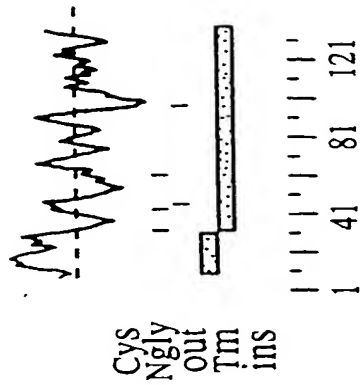


Fig. 11Y-6

GTCGACCCAC	CGGTCCGGTT	TGCTTGGAGA	TGCTGCTAAA	ACAGAGAGGC	TGTGAACAAG	60
GACATTACCG	AGCAGGAGCA	TACATTGAGA	AGACAAGGAG	CCCTGCTCGC	TGCACCCGAAT	120
ATCTTATCAA	AAAGACTCCT	ATCTGTATGC	CAACCCAGAC	TTCCAGAAAG	AGATCAGATC	180
CCTGAATCCC	CATCATC	ATG AAC	TGG CAC	ATG ATC	TCG GGG CTT ATC	230
	Met Asn	Trp His	Met Ile	Ile Ser	Gly Leu Ile	
	1	5	10			
GTA GTA	GTG ATC	AAA GTT	GTT GGA	ATG ACC	TTT TTT CTG CTG TAT TTC	278
Val Val	Val Ile	Lys Val	Val Val	Gly Met	Thr Phe Phe Leu Leu Tyr Phe	
	15	20	25			
CCA CAG	GTT TTT	GGC AAA	AGT AAT	GAT GGC	TTC GTC CCC ACG GAG AGC	326
Pro Gln	Val Phe	Gly Lys	Ser Ser	Asn Asp	Gly Phe Val Pro Thr Glu Ser	
	30	35	40			
TAC GGA	ACC ACT	AGT GTG	CAG AAT	GTC TCA	CAG ATC TTT GGG AGA AAT	374
Tyr Gly	Thr Thr	Ser Val	Gln Val	Asn Val	Ser Gln Ile Phe Gly Arg Asn	
	45	50	55			
GAC GAA	AGT ACC	ATG CCT	ACA AGG	AGC TAT	GGA ACA GTC TGT CCC AGA	422
Asp Glu	Ser Thr	Met Pro	Thr Thr	Arg Ser	Tyr Gly Thr Val Cys Pro Arg	
	60	65	70			
AAC TGG	GAT TTT	CAC CAA	GGA AAA	TGC TTT	TTC TTC TCC TTC TCC GAA	470
Asn Trp	Asp Phe	His Gln	Gly Lys	Cys Phe	Phe Ser Phe Ser Glu	
	80	85	90			

Fig. 11Z-1

TCA CCT TGG AAA GAC AGC ATG GAT TAT TGT GCA ACA CAA GGA TCC ACA	518
Ser Pro Trp Lys Asp Ser Met Asp Tyr Cys Ala Thr Gln Gly Ser Thr	
95 100 105	
CTG GCA ATT GTC AAC ACT CCA GAG AAA CTG AAG TAT CTT CAG GAC ATA	566
Leu Ala Ile Val Asn Thr Pro Glu Lys Leu Tyr Leu Gln Asp Ile	
110 115 120	
GCT GGT ATT GAG AAT TAC TTT ATT GGT TTG GTA CGT CAG CCT GGA GAG	614
Ala Gly Ile Glu Asn Tyr Phe Ile Gly Leu Val Arg Gln Pro Gly Glu	
125 130 135	
AAA AAG TGG CGC TGG ATC AAC AAC TCT GTG TTC AAT GGC AAT GTT ACC	662
Lys Lys Trp Arg Trp Ile Asn Asn Ser Val Phe Asn Gly Asn Val Thr	
140 145 150 155	
AAT CAG GAC CAG AAC TTC GAC TGT GTC ACT ATA GGT CTG ACG AAG ACA	710
Asn Gln Asp Gln Asn Phe Asp Cys Val Thr Ile Gly Leu Thr Lys Thr	
160 165 170	
TAT GAT GCT GCA TCA TGT GAA GTC AGC TAT CGC TGG ATC TGC GAA ATG	758
Tyr Asp Ala Ala Ser Cys Glu Val Ser Tyr Arg Trp Ile Cys Glu Met	
175 180 185	

Fig. 11Z-2

807

AAT GCC AAA TGATCATAGA TCTCTACAAG AGTGAATTTT TACAGAGCTA

Asn Ala Lys

190

867

GCAAAGGAGA TTAGTTGTGA CTGAAACCAG CCCAGGAAAT ATAGAGCATC AAAGACTGTG

927

CCCATCTTCC ATAGGTGGAG TTCCCTATTG AATCCTCAA GTCAATTTGT TACTCCACAA

987

ACATCTTCAC ATAGTAAAC TCCCTTTCTG ACCAAGTATT CCTAAGACC ACACTTCCTG

1047

TGAGAGGGGA CTGGATTCTA GTTATCTGCA GACAGAGCCA GGATTCTGGA GATGAAATCA

1107

ATATGGAAAT GCAGTCTGTT TCTGTAGAGC TGAGCCTTTT AACTAATCAG TAGGGTTTTG

1167

TCTGTTGTCA GAACTGTTTG ATCCTTAGAG AACATGCCCA CGCCACTGAG GAGAAACTGC

1227

TCGTGGAACA GATATGAGAA CTGTTAGGAA GCACTATGGG CAGAAGAATA TAAACTTGGC

1287

TTACACAACAT CCCCATTCC AGAAAGCCTC CCATTCCCAT ACAACATCGT AGAAGCAGAG

1347

GTCCTTCTGA ATTGGGGAAG GACCTCTACA GCTCGACTTG GTACTGAACA AATATTGAGG

1407

GAATGAAGAA AGTTCTGAAT AGGACAGAGA TAAACAAGGA GGAGAAGGAA AGAGATAGGA

1467

AGAAAGGAGA AGTGGGAAG AGGGGAAAA GGAATGATGG GCAGGAGAAA AAGAGACAGG

1527

AGCAGCCAGG AAAAACTC AAGCTAAATT TTTTTCAGGT TTTGGATAAA ATCTATTGTG

1587

ACATAAATAA TATCTTTTCA TTAGAAGAGA AAAGGCAAAA TTGGGACAA ATGGGCACCA

1647

TGAGAGATGA AGCAGAGGTT AATTTGATCA CAAGGAAAGA AGGCAGGAA TGAGGTTGAA

1707

AACTTTTGG ATACCTTGGC TGTATCTCA AGAAGGTACA AGCTGCATAA AGTATAGGAG

1767

AAAAGAGATG TGCTGGTTGT TTTAAGTAGC AAAAATTAAA CTACAGAGAA GCCTATAGAA

1827

AGCTAAAGGA ATTAAACCA TCCAATAATC AATTCATTAT TTTCAACTAA TAGCAATATG

1887

TATGTGCATT ACTAGTCAAA ATAAATTGTG AATTCTGTTA TTATAAAAAA AAAAAAAAAG

1896

GGCGGCCGC

Fig. 11Z-3

MI289	ATGAACTGGCACATGATCATCTCGGGGCTTATCGTAGTAGTCAAAAGTTGTTGGAATG	60
HI289	ATGAACTGGCACATGATCATCTCGGGCTTATGTGGTAGTGCTTAAAGTTGTTGGAATG	60
MI289	ACCTTTTCTGCTGTATTTCCACAGGTTTGTGGCAAAAGTAATGATGGCTTCGTCCCC	120
HI289	ACCTTATTCTACTTTATTTCCACAGATTTTAAACAAAAGTAACGATGGTTTCACCACC	120
MI289	ACGGAGAGCTACGGAACCACTAGTGTGCAGAAATGTCTCACAGATCTTTGGGAGAGAAATGAC	180
HI289	ACCAGGAGCTATGGAACA-----GTCTCACAGATTTTGGGAGCAGTTCCCCAAGTCCC	174
MI289	GAAAGTACCATGCCACAGGAGCTATGGAACAGTCTGTCCCAAGAACTGGGATTTTCAC	240
HI289	AACGGCTTCATTACCACAGGAGCTATGGAACAGTCTGCCCCCAAAGACTGGGAAATTTTAT	234
MI289	CAAGGAAAATGCTTTTCTTCTCCTTCTCCGAATCACCTTGGAAAGACAGCATGGATTAT	300
HI289	CAAGCAAGATGTTTTTCTTATCCACTCTCTGAATCATCTTGGAAATGAAGCAGGGACTTT	294

Fig. 11Z-4

MI289	TGTGCAACACAAGGATCCACACTGGCAATTGTCAACACTCCAGAGAAACTGAAAGTATCTT	360
HI289	TGCAAAAGGAAAAGGATCCACATTTGGCAATTGTCAACACGCCAGAGAAACTGAAAGTTTCTT	354
MI289	CAGGACATAGCTGGTATTGAGAATTACTTTATTGGTTTGGTACGTCAGCCCTGGAGAGAAA	420
HI289	CAGGACATAAAGTATGAGAAAGTATTTTATTGGCTTAAATTACCATCGTGAAGAGAGAAA	414
MI289	AAGTGGCGCTGGATCAACAACCTCTGTGTTCAATGGCAATGTTACCAATCAGGACCAGAAC	480
HI289	AGGTGGCGTTGGATCAACAACCTCTGTGTTCAATGGCAATGTTACATCATCCAATCAGAAT	474
MI289	TTCGACTGTGTCACTATAGGTCTGACGAAGACATATGATGCTGCATCATGTGAAGTCAGC	540
HI289	CAGAAATTCAACTGTGCGACCATTGGCCCTAACAAAGACATTTGATGCTGTGACATCAGC	534
MI289	TATCGCTGGATCTGCGAAATGAATGCCCAA	570
HI289	TACCGCAGGATCTGTGAGAAGAATGCCCAA	564

Fig. 11Z-5

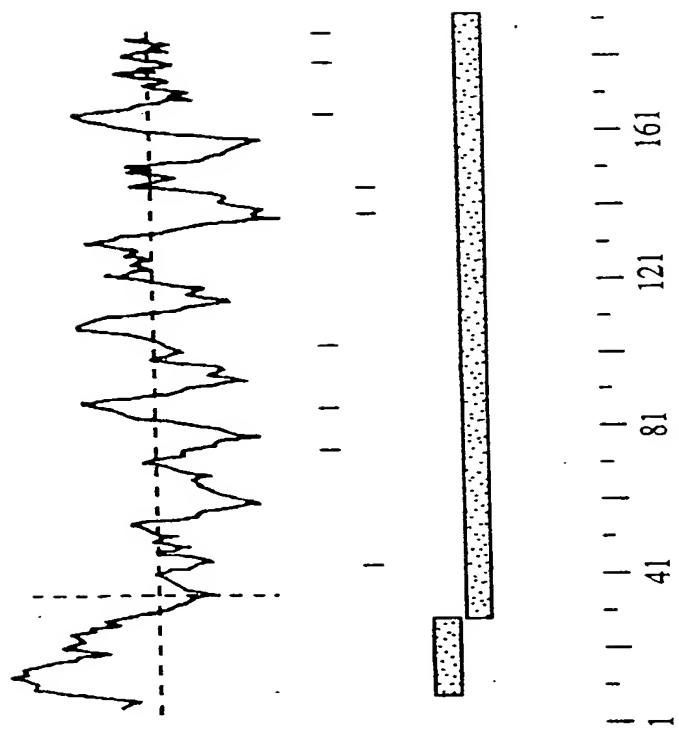


Fig. 11Z-6

L	F	L	G	G	V	G	M	V	G	T	V	A	V	T	V	M	P	Q	19	
G	CTG	TTT	CTT	GGT	GGT	GTT	GGA	ATG	GTG	GGC	ACA	GTG	GCT	ACT	GTC	ATG	CCT	CAG	58	
W	R	V	S	A	F	I	E	N	N	I	V	V	F	E	N	F	W	E	G	39
TGG	AGA	GTG	TCG	GCC	TTC	ATT	GAA	AAC	AAC	ATC	ATC	GTG	GTT	TTT	GAA	AAC	TTC	TGG	GAA	118
L	W	M	N	C	V	R	Q	A	N	I	R	M	Q	C	K	I	Y	D	S	59
CTG	TGG	ATG	AAT	TGC	GTG	AGG	CAG	GCT	AAC	ATC	ATC	AGG	ATG	CAG	TGC	AAA	ATC	TAT	GAT	178
L	L	A	L	S	P	D	L	Q	A	A	R	G	L	M	C	A	A	S	V	79
CTG	CTG	GCT	CTT	TCT	CCG	GAC	CTA	CAG	GCA	GCC	AGA	GGA	CTG	ATG	TGT	GCT	GCT	TCC	GTG	238
M	S	F	L	A	F	M	M	A	I	L	G	M	K	C	T	R	C	T	G	99
ATG	TCC	TTC	TTG	GCT	TTC	ATG	ATG	GCC	ATC	CTT	GGC	ATG	AAA	TGC	ACC	AGG	TGC	ACG	GGG	298
D	N	E	K	V	K	A	H	I	L	L	T	A	G	I	I	F	I	I	T	119
GAC	AAT	GAG	AAG	GTG	AAG	GCT	CAC	ATT	CTG	CTG	ACG	GCT	GGA	ATC	ATC	TTC	ATC	ATC	ACG	358
G	M	V	V	L	I	P	V	S	W	V	A	N	A	I	I	R	D	F	Y	139
GGC	ATG	GTG	GTG	CTC	ATC	CCT	CTC	ATC	AGC	TGG	GTT	GCC	AAT	GCC	ATC	ATC	AGA	GAT	TTC	418
N	S	I	V	N	V	A	Q	K	R	E	L	G	E	A	L	Y	L	G	W	159
AAC	TCA	ATA	GTG	AAT	GTT	GCC	CAA	AAA	CGT	GAG	CTT	GGA	GAA	GCT	CTC	TAC	TTA	GGA	TGG	478

Fig. 12A

T	T	A	L	V	L	I	V	G	G	A	L	F	C	C	V	C	N	179		
ACC	ACG	GCA	CTG	GTG	CTG	ATT	GTT	GGA	GGA	GCT	CTG	TTC	TGC	TGC	GTT	TTT	TGT	TGC	AAC	538
E	K	S	S	S	Y	R	Y	S	I	P	S	H	R	T	T	Q	K	S	Y	199
GAA	AAG	AGC	AGT	AGC	TAC	AGA	TAC	TCG	ATA	CCT	TCC	CAT	CGC	ACA	ACC	CAA	AAA	AGT	TAT	598
H	T	G	K	K	S	P	S	V	Y	S	R	S	Q	Y	V	*				215
CAC	ACC	GGA	AAG	AAG	TCA	CCG	AGC	GTC	TAC	TCC	AGA	AGT	CAG	TAT	GTG	TAG				649
TTG	TG	TAT	G	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	728
AGAA	ACT	TTT	G	AT	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	807
TAT	TT	CAG	CAG	AA	TG	AG	ATA	TG	TT	TG	AT	TG	TT	CT	AG	AA	TG	TT	TT	886
AAG	CA	TCT	ACT	TT	TAT	CA	TT	TCT	AA	AG	CA	TG	CA	TT	TT	TCT	AA	TT	TT	965
GAC	AT	AG	CA	TAT	AG	AT	AG	CA	TAT	AG	CA	TAT	AG	CA	TAT	AG	CA	TAT	AG	1044
AA	TG	CC	AG	TC	CA	TAT	AG	CA	TAT	AG	CA	TAT	AG	CA	TAT	AG	CA	TAT	AG	1123
TAC	TAT	AA	TG	TT	TAA	AA	CAG	CT	TAG	GG	AT	TAA	TG	CT	TCC	AT	TAA	TG	CT	1202
CAT	TG	TAA	AG	GA	AA	TG	AA	TG	AA	TG	AA	TG	AA	TG	AA	TG	AA	TG	AA	1281
TT	CT	CC	CAG	AG	CT	TT	TT	TT	TT	TT	TT	TT	TT	TT	TT	TT	TT	TT	TT	1360
TC	AA	CT	G	CT	TT	TCC	AGG	CT	AT	CT	CA	AG	AA	AG	TG	AT	AG	AA	AG	1439
AA	AT	AT	TT	TG	TAT	TT	TG	AT	TT	TG	AT	TT	TG	AT	TT	TG	AT	TT	TG	1518
AG	TAT	TG	AG	TAC	AG	CT	TT	TG	AG	CT	TT	TG	AG	CT	TT	TG	AG	CT	TT	1597

Fig. 12B

CCAAAAACAACAAAAAAGTTGTCCCTTTGAGAACTTCACCTGCTCCTATGTGGGTACCTGAGTCAAAATTGTCA 1676
TTTTTGTTCGTGAAAAAATAAATTTCCCTTCTTGTACCAATTTCTGTTTAGTTTTTACTAAAAATCTGTAAATACTGTATTTT 1755
TCTGTTTATTCCAAATTTGATGAAACTGACAATCCAATTTGAAAGTTTGTGTCGACGCTGTCTAGCTTAAATGAATGT 1834
GTTCTATTTGCTTTATACATTTATATATAATAAATTGTACATTTTCTAAAAAATAAAAAAATAAAAAAATAAAAAA 1909

Fig. 12C

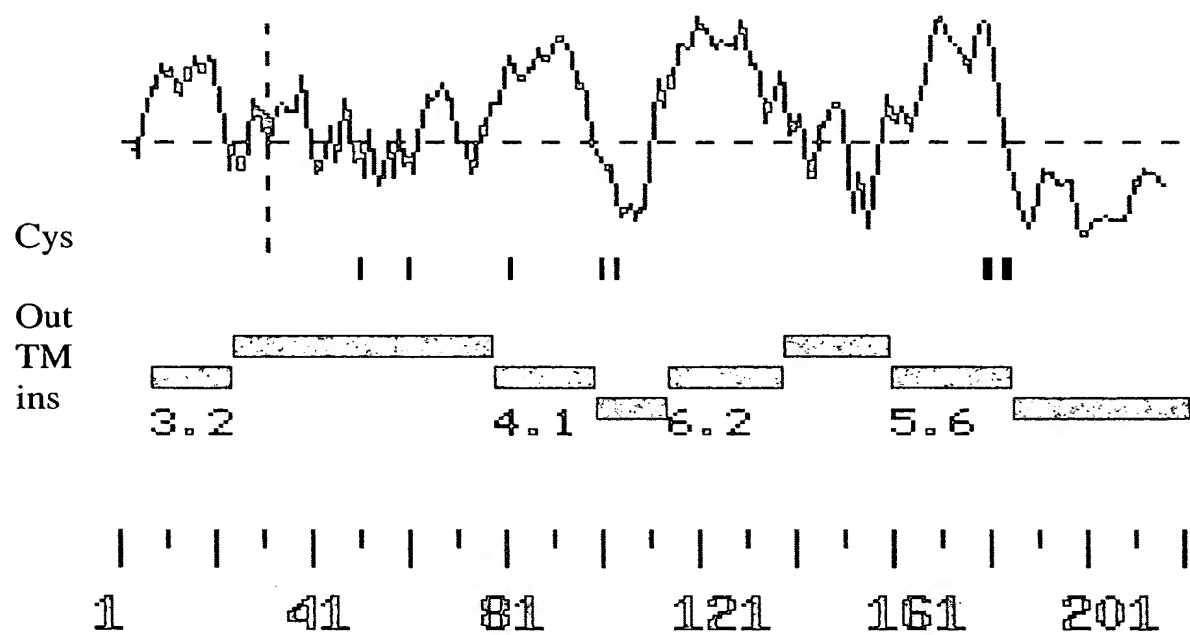


Fig. 12D

[illegible]

Fig. 12E

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DKFZ -----
I309 TCATCACGGGCA TGGTGCTCATCCCTGTGAGCTGGGTGCCAATGCCATCATCAGAGATTTCTATAA
      360      370      380      390      400      410      420
DKFZ -----
I309 CTCAATAGTGAATGTTGCCCCAAAAACGTGAGCTTGGAGAAAGCTCTCTACTTAGGATGGACCACGGCACTG
      430      440      450      460      470      480      490
DKFZ -----
I309 GTGCTGATTGTTGGAGGAGCTCTGTTCTGCTGCGTTTTTTGTGCAACGAAAAGACGAGTAGCTACAGAT
      500      510      520      530      540      550      560
DKFZ -----
I309 ACTCGATA CCTTCCCATCGCACAAACCCAAAAAGTTATCACACCCGGAAGAAGTCACCGAGCGTCTACTC
      570      580      590      600      610      620      630
DKFZ -----
I309 CAGAAGTCAGTATGTGTAGTTGTGTATGTTTTTTTAAC TTACTATAAAGCCAATGCAAAATGACAAAAATC
      640      650      660      670      680      690      700

```

Fig. 12F

170	180	190	200	210	220	230
DKFZ	ACATAGATGAGTGTAACATTTATATCTCACATAGAGACATGCTTATATGGTTTATTATTTAAAAATGAAATGC					
	::					
I309	ACATAGATGAGTGTAACATTTATATCTCACATAGAGACATGCTTATATGGTTTATTATTTAAAAATGAAATGC					
990	1000	1010	1020	1030	1040	1050
240	250	260	270	280	290	300
DKFZ	CAGTCCATTACACTGAATAAATAGAACTCAACTATTGCTTTTCAGGGAAATCATGGATAGGGTTGAAGAA					
	::					
I309	CAGTCCATTACACTGAATAAATAGAACTCAACTATTGCTTTTCAGGGAAATCATGGATAGGGTTGAAGAA					
1060	1070	1080	1090	1100	1110	1120
310	320	330	340	350	360	370
DKFZ	GGTTACTATTAAATTGTTTTAAAAACAGCTTAGGGATTAAATGTCTCCCATTTATAATGAAGATTAAAAATGA					
	::					
I309	GGTTACTATTAAATTGTTT-AAAAACAGCTTAGGGATTAAATGTCTCCCATTTATAATGAAGATTAAAAATGA					
1130	1140	1150	1160	1170	1180	
380	390	400	410	420	430	440
DKFZ	AGGCTTTAATCAGCATTTGTAAAGGAAATTGAATGGCTTTCTGATATGCTGTTTTTTTAGCCTTAGGAGTTAG					
	::					
I309	AGGCTTTAATCAGCATTTGTAAAGGAAATTGAATGGCTTTCTGATATGCTGTTTTTTTAGCCTTAGGAGTTAG					
1190	1200	1210	1220	1230	1240	1250

Fig. 12H

450	460	470	480	490	500	510
DKFZ	AAATCCCTAACTTCTTTATCCTCTTCTCTCCAGAGGCCTTTT	TTTCTTCTTGTGTATTAATTAACATTTTTAA				

I309	AAATCCCTAACTTCTTTATCCTCTTCTCTCCAGAGGCCTTTT	TTTCTTCTTGTGTATTAATTAACATTTTTAA				
1260	1270	1280	1290	1300	1310	1320
520	530	540	550	560	570	580
DKFZ	AAAGCAGATATTTTGTCAAGGGGCTTTTGCAATTCAAACTGCTTT	TCCAGGGCTATACTCAGAAAGAAAGATA				

I309	AAAGCAGATATTTTGTCAAGGGGCTTTTGCAATTCAAACTGCTTT	TCCAGGGCTATACTCAGAAAGAAAGATA				
1330	1340	1350	1360	1370	1380	1390
590	600	610	620	630	640	650
DKFZ	AAAGTGTGATCTAAGAAAAAGTGATGGTTTTTAGGAAAGTGAAAA	TATTTTGTGTATTTGAAGAAG				

I309	AAAGTGTGATCTAAGAAAAAGTGATGGTTTTTAGGAAAGTGAAAA	TATTTTGTGTATTTGAAGAAG				
1400	1410	1420	1430	1440	1450	1460
660	670	680	690	700	710	720
DKFZ	AATGATGCATTTTGACAAGAAATCATATATGTATGGATATATTT	TAAATAAGTATTTGAGTACAGACTTTG				

I309	AATGATGCATTTTGACAAGAAATCATATATGTATGGATATATTT	TAAATAAGTATTTGAGTACAGACTTTG				
1470	1480	1490	1500	1510	1520	1530

Fig. 12I

730	740	750	760	770	780	790
DKFZ	AGGTTTCATCAATATAATAAAGAGCAGAAAAATATGTCCTTGGTTTTCATTTGCTTACCAAAAAACAA					
	::					
I309	AGGTTTCATCAATATAATAAAGAGCAGAAAAATATGTCCTTGGTTTTCATTTGCTTACCAAAAAACAA					
1540	1550	1560	1570	1580	1590	1600
800	810	820	830	840	850	860
DKFZ	CAACAAAAAGTTGTCCCTTTGAGAACTTCACCTGCTCCTATGTGGGTACCTGAGTCAAAATTGTCATTT					
	::					
I309	CAACAAAAAGTTGTCCCTTTGAGAACTTCACCTGCTCCTATGTGGGTACCTGAGTCAAAATTGTCATTT					
1610	1620	1630	1640	1650	1660	1670
870	880	890	900	910	920	930
DKFZ	TTGTTCTGTGAAAAATAAAATTTCCCTTCTTGTAACCATTTCTGTTAGTTTACTAAAAATCTGTAAATACTG					
	::					
I309	TTGTTCTGTGAAAAATAAAATTTCCCTTCTTGTAACCATTTCTGTTAGTTTACTAAAAATCTGTAAATACTG					
1680	1690	1700	1710	1720	1730	1740
940	950	960	970	980	990	1000
DKFZ	TATTTTCTGTATTATCCAAATTTGATGAAACTGACAATCCAATTTGAAAGTTTGTGTCGACGTCGTCT					
	::					
I309	TATTTTCTGTATTATCCAAATTTGATGAAACTGACAATCCAATTTGAAAGTTTGTGTCGACGTCGTCT					
1750	1760	1770	1780	1790	1800	1810

Fig. 12J

1010	1020	1030	1040	1050	1060	1070
DKFZ	AGCTTAAATGAATGTTCTATT	TGCTTTATACATTATTAATAAATTGTACATTTT	TCCAAAAAAA			
	::					
I309	AGCTTAAATGAATGTTCTATT	TGCTTTATACATTATTAATAAATTGTACATTTT	TCTAAAAAAA			
1820	1830	1840	1850	1860	1870	1880
1080	1090					
DKFZ	AAAAAAA	-----				
	::::::::::::					
I309	AAAAAAA	AAAAAAA				
1890	1900					

Fig. 12K

I309	G-----CTGTTTCTTGGTGTGTGGAATGGTGGCACAGTGGCTG	10	20	30	40	50	60	70
CLAUD8	ATGGCAACCTACGCTCTTCAAATGGCTGCACCTGGTGTGTGGCATGGTGGGCACGGTGGCTG	80	90	100	110	120	130	140
I309	TCACTGTTCATGCCCTCAGTGGAGAGTGTGCGCCCTTCATTGAAAAACAACATCGTGGTTTTGTGAAAACTTCTG	120	130	140	150	160	170	180
CLAUD8	TGACTATCATGCCCTCAGTGGAGAGTGTCTGCCCTTCATCGAAAGTAACATTTGTGGTGTTTTGAGAACCGCTG	150	160	170	180	190	200	210
I309	GGAAGGACTGTGGATGAATTGCGTGAGGCAGGCTAACATCAGGATGCAGTGCAAAAATCTATGATTCCCTG	190	200	210	220	230	240	250
CLAUD8	GGAAGGCTTGTGGATGAATTGTATGAGGCATGCCAACATCAGAATGCAGTGCAGGTCTACGACTCCCTG	220	230	240	250	260	270	280
I309	CTGGCTCTTTCTCCGACCTACAGGCAGCCAGAGGACTGATGTGTGCTGCTTCCGTGATGTCTCTTCTTGG	260	270	280	290	300	310	320
CLAUD8	CTGGCTCTTAGTCCAGACCTCCAGGCATCCCAGGACTGATGTGTGCTGCGTCCGTCTTGGCTTTCTTGG	300	310	320	330	340	350	360

Fig. 12L

I309	CTTTCATGATGCCCATCCTTGGCATGAAATGCACCAGGTGCACGGGGACAAATGAGAAGGTGAAGGCTCA	260	270	280	290	300	310	320
CLAUD8	CTTTCATGACAGCCATCCTCGGAATGAAGTGCACCAGATGCACGGGGACGATGAGAACCTGAAGAGCCG	290	300	310	320	330	340	350
I309	CATTCTGCTGACGGCTGGAATCATCTTTCATCATCAGGCGCATGGTGGTCTCATCCCTGTGAGCTGGGTT	330	340	350	360	370	380	390
CLAUD8	CATCTTGCTGACAGCCGGAATCATCTTCTTCATCACCGGCTTGGTTGTGCTCATCCCTGTGAGCTGGGTT	360	370	380	390	400	410	420
I309	GCCAAATGCCCATCATCAGAGATTTCATAAAGTCAATAGTGAATGTGCCCAAAACGTGAGCTTGGAGAAG	400	410	420	430	440	450	460
CLAUD8	GCCAAATTCATCATCAGAGACTTCTACAACCCACTGGTGGATGTGGCCCTAAAGCCGAGCTGGGAGAAG	430	440	450	460	470	480	490
I309	CTCTCTACTTAGGATGGACCACGGCAGCTGGTGTGCTGATTGTTGGAGGAGCTCTGTTCTGCTGCGTTTTTG	470	480	490	500	510	520	530
CLAUD8	CCCTCTACATAGGCTGGACCACAGCGCTGGTGTGATCGCTGGAGGAGCACTGTTCTGTGTGTTTTTG	500	510	520	530	540	550	560

Fig. 12M

```

540      550      560      570      580      590      600
I309 TTGCAACGAAAGAGCAGTAGCTACAGATACTCGATACCTTCCCATCGCACAAACCCAAAAAGTTATCAC
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CLAUD8 TTGTACTGAAAGGAGCAACAGTTACAGGTACTCGGTACCATCCCATCGCACCACTCAACGGAGTTTCCAC
570      580      590      600      610      620      630
      610      620      630      640      650      660      670
I309 ACCGGAAAGAGTCACCGAGCGTCTACTCCAGAAGTCAAGTATGTGTAGTTGTGTATGTTTTTAACTTT
      . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
CLAUD8 GCCGAAAAGAGATCTCCGAGCATATATACTCCAAAAGTCAGTATGTGTAG-----
640      650      660      670
      680      690      700      710      720      730      740
I309 ACTATAAGCCATGCAAATGACAAAAATCTATATTACTTCTCAAAATGGACCCCAAGAACTTTGATT
CLAUD8 -----
      750      760      770      780      790      800      810
I309 TACTGTTCTTAACTGCCTAATCTTAATTACAGGAACGTGTGCATCAGCTATTTATGATTCATATAAGCTATT
CLAUD8 -----

```

Fig. 12N

	820	830	840	850	860	870	880
I309	TCAGCAGAA	TGAGATAT	TAAACCA	TGCTTT	GATTGTT	CTAGAAA	GTATAGTAA
							TTTGTCTTAAGGT
CLAUD8	-----						
	890	900	910	920	930	940	950
I309	GGTTCAAG	CATCTCT	TTTTTAT	CACTTT	CAAAATG	ACATTTG	CTAAAGACT
							GCATTATTTTACTAC
CLAUD8	-----						
	960	970	980	990	1000	1010	1020
I309	TGTAATT	CTCCAG	CATAGCA	TATATG	TACATAG	ATGAGTG	TAAACATTTATATCT
							CACATAGAGACATG
CLAUD8	-----						
	1030	1040	1050	1060	1070	1080	1090
I309	CTTATAT	GGTTTT	TATTTAA	AAATGAA	ATGCCAG	TCCATTAC	ACTGAATAAGAACT
							CAACTATTGCTTT
CLAUD8	-----						
	1100	1110	1120	1130	1140	1150	1160
I309	TCAGGAA	AATCAT	GGTAGG	GTGAAG	AAGGTT	ACTATT	AATGTTTAAAAACAGCT
							TAGGGATTAAATGT
CLAUD8	-----						

Fig. 120

	1170	1180	1190	1200	1210	1220	1230
I309	CCTCCATTTATAATGAAGATTAAATGAAGCCTTTAATCAGCATTTGTAAAGGAAATTGAAATGGCTTTCTG						
CLAUD8	-----						
	1240	1250	1260	1270	1280	1290	1300
I309	ATATGCTGTTTTTAGCCTAGGAGTTAGAAATCCTAACTTCTTTATCCTCTTCTCCAGAGGCTTTTTTTT						
CLAUD8	-----						
	1310	1320	1330	1340	1350	1360	1370
I309	TTCTTGTTGTTAAATTAACATTTTTTAAAAAGCAGATATTTTGTCAAGGGGCTTTGCATTCAAAACGTGCTT						
CLAUD8	-----						
	1380	1390	1400	1410	1420	1430	1440
I309	TTCCAGGGCTATACTCAGAAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATGGTTTTAGGAAAGTGAA						
CLAUD8	-----						

Fig. 12P

	1450	1460	1470	1480	1490	1500	1510
I309	AATATTTTGTGTAATTTGAAGAAGAAATGATGCATTTTGGACAAAGAAATCATATATGTATGGATATAT						
CLAUD8	-----						
	1520	1530	1540	1550	1560	1570	1580
I309	TTTAAATAAGTATTTGAGTACAGACTTTGAGGTTTCATCAATATAATAAAGAGCAGAAAAATATGTCTT						
CLAUD8	-----						
	1590	1600	1610	1620	1630	1640	1650
I309	GGTTTTCATTTGCTTACCATAAAACAAACAAAAAGTTGTCTTTTGAGAACTTCACCTGCTCCTAT						
CLAUD8	-----						
	1660	1670	1680	1690	1700	1710	1720
I309	GTGGGTACCTGAGTCAAAATTGTCAATTTTGTCTGTGAAAAATAAATTCCTTCTTGTAACCATTTCTGT						
CLAUD8	-----						
	1730	1740	1750	1760	1770	1780	1790
I309	TTAGTTTACTAAAAATCTGTAAATACTGTATTTTCTGTATTATTCCAAATTTGATGAAACTGACAATCCA						
CLAUD8	-----						

Fig. 12Q

	1800	1810	1820	1830	1840	1850	1860
I 309	ATTGAAAGTTTGTGTCGACGCTGTCTAGCTTAAATGAATGTGTTCTATTTCCTTTATACATTTATATT						
CLAUD8	-----						
I 309	AATAAATTGTACATTTTCTAAAAAATAAAAAAAAAAAAAA						
CLAUD8	-----						

Fig. 12R

	10	20	30	40	50	60	70
CLAUD8	MATYALQMAALVLGGVGMVGTVAVTIMPQWRVSAFIESNIVVFENRWEGLWMNCMRHANIRMQCKVYDSL						
	:	:	:	:	:	:	:
I309	-----LFLGGVGMVGTVAVTMPQWRVSAFIENNIVVFENFWEGLMNCVQRQANIRMQCKIYDSL	10	20	30	40	50	60
	80	90	100	110	120	130	140
CLAUD8	LALSPDLQASRGLMCAASVLAFLAFMTAILGMKCTRCTGDDENVKSRILLTAGIIFFITGLVVLIPVSWV						
	:	:	:	:	:	:	:
I309	LALSPDLQAARGLMCAASVMSFLAFMTAILGMKCTRCTGDNEKVKAHILLTAGIIFITGMVVLIPVSWV	70	80	90	100	110	120
	150	160	170	180	190	200	210
CLAUD8	ANSIIRDFYNPLVDVALKRELGEALYIGWTTALVLIAGGALFCCVFCCTERSNSYRYSVPSHRTTQRSFH						
	:	:	:	:	:	:	:
I309	ANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVFCCKNEKSSSYRYSIPSHRTTQKSYH	140	150	160	170	180	190
	220						
CLAUD8	AEKRSPSIYSKSQYV						
	.	:	:	:	:	:	:
I309	TGKKSPSVYSRSQYV						
	210						

Fig. 12S

I309LFLGGVGMVGTVAVTMPQWRVSAFIENNIVVFENFWEGL 40
 hCPE MASMGLQVMGIALAVLGWLAVMLCCALPMWRVTAFIGSNIIVTSQTIWEGL 50
 mCPE MASMGLQVLGISLAVLGWLGIILSCALPMWRVTAFIGSNIIVTAQTSWEGL 50
 rRPV .MSMSLEITGTSLAVLGWLCTIVCCALPMWRVSAFIGSSIIITAQITWEGL 49

 I309 WMNCVRQANIRMQCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAIL 90
 hCPE WMNCVVQSTGMQCKVYDSLALPQDLQAARALVISIIVAALGVLLSVV 100
 mCPE WMNCVVQSTGMQCKMYDSLALPQDLQAARALMVISIIVGALGMLLSVV 100
 rRPV WMNCV.QSTGMQCKMYDSLALPQDLQAARALIVVSILLAAFGLLVALV 98

 I309 GMKCTRCTGDNEKVKAHILLTAGIIFIITGMVVLIPVSWVANAIIRDFYN 140
 hCPE GGKCTNCLED.ESAKAKTMIVAGVVFLLAGLMVIVPVSWTAHNI IQDFYN 149
 mCPE GGKCTNCMED.ETVKAKIMITAGAVFIVASMLIMVPVSWTAHNVIRDFYN 149
 rRPV GAQCTNCVQD.ETAKAKITIVAGVLFLLAAVLTLPVSVWSANTIIRDFYN 147

 I309 SIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVCCNEKSSSYRYSIP 190
 hCPE PLVASGQKREMGASLYVGWAAAGLLLLGGGLCC.NCPRTDKPYSAKYS 198
 mCPE PMVASGQKREMGASLYVGWAAAGLLLLGGGLCCSCPPRSNDKPYSAKYS 199
 rRPV PLVPEAQKREMGTGLYVGWAAAALQLLGGALLCCSCPPREKYAPTILYS 197

 I309 SHRTTQKSYHTGKKSPSVYSRSQYV 215
 hCPE AARSAASNYV..... 209
 mCPE AARSVPASNYV..... 210
 rRPV APRSTGPGTGTAYDRKTTSERPGARTPHHHYQPSMYPTRPACSLASET 248

Fig. 12T

CGAGCGGCGCGCGG	CAGGTCAGACATGGGCCAAGGAGCCAGAGCCGTCGCGGGTCTGTGAGTTGAGCTTGAGGCCG	79																		
M	R	V	I	M	G	I	A	S	L	G	F	L	W	A	V	F	L	18		
CAGG	ATG	AGG	GTC	ATC	ATG	GGG	ATA	GCC	AGC	CTG	GGG	TTC	CTC	TGG	GCA	GTA	TTC	CTG	137	
L	P	L	V	F	G	V	P	T	E	E	T	T	F	G	E	S	V	A	S	38
CTT	CCT	CTT	GTG	TTT	GGG	GTC	CCC	ACA	GAG	GAG	ACT	ACC	TTT	GGA	GAA	TCT	GTG	GCC	TCC	197
H	L	P	K	G	C	R	R	C	C	D	P	E	D	L	M	S	S	D	D	58
CAT	CTC	CCC	AAA	GGC	TGT	CGA	CGA	TGC	TGT	GAC	CCC	GAG	GAC	CTG	ATG	TCC	TCT	GAT	GAT	257
T	V	Q	A	P	V	S	P	Y	V	L	P	E	V	R	P	Y	L	G	R	78
ACG	GTC	CAG	GCC	CCT	GTT	TCC	CCT	TAT	GTC	CTG	CCT	GAA	GTC	AGG	CCG	TAC	CTC	GGC	CGC	317
D	H																		80	
GAC	CAC																		323	

Fig. 13A

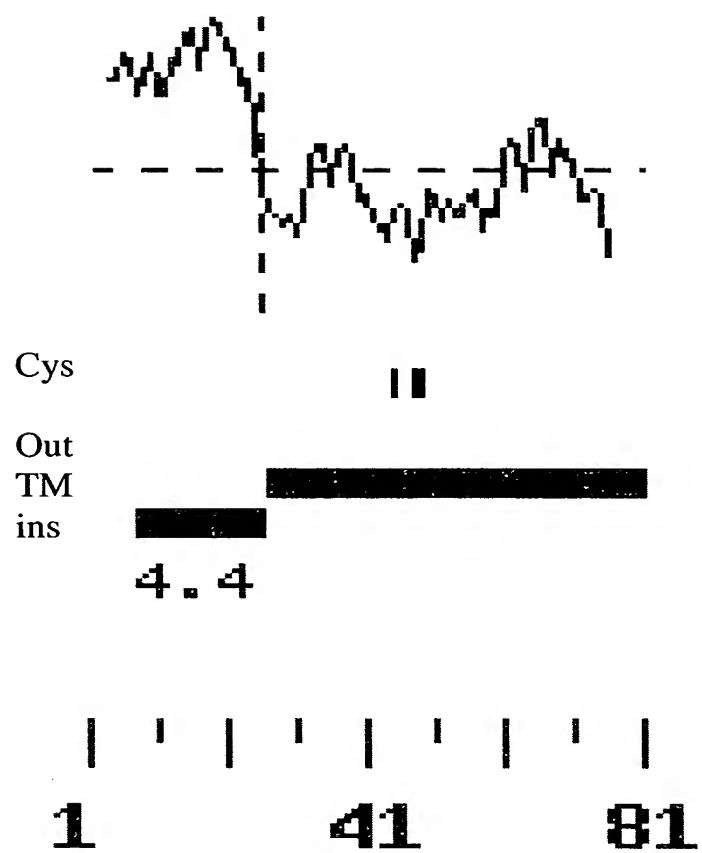


Fig. 13B

[illegible]

Fig. 14A

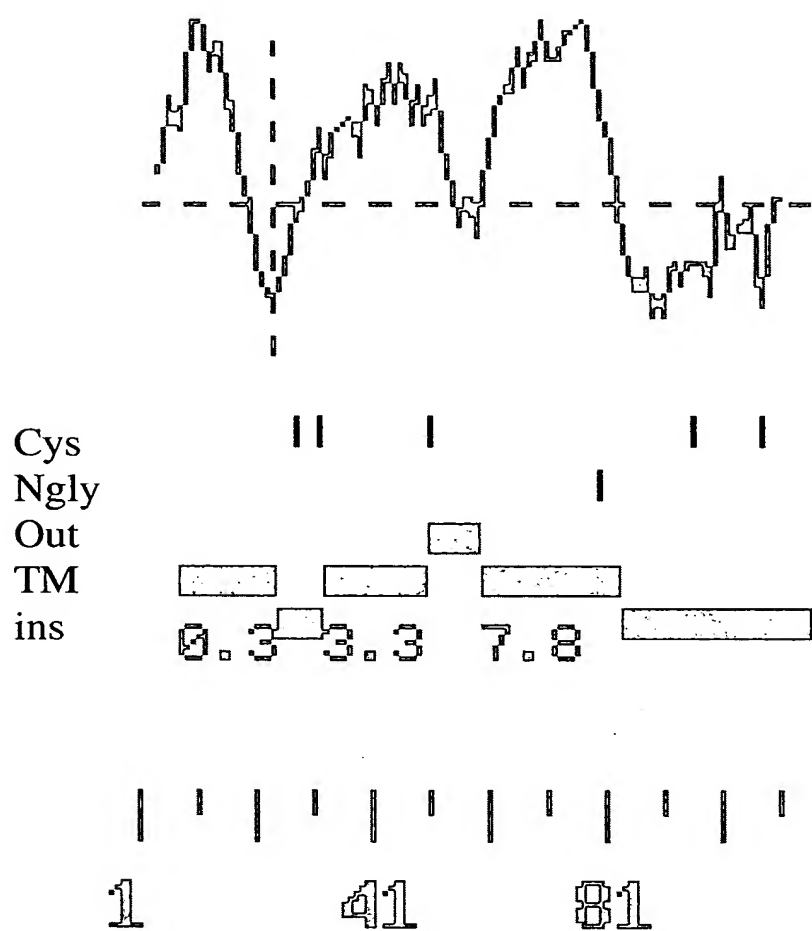


Fig. 14B

I S K G I A D I M I A F R T R V H G R C	168
ATT TCA AAG GGG ATT GCA GAC ATC ATG ATG ATT GCC TTT AGG ACT CGA GTC CAT GGT CGG TGT	548
P R Y F D G G P L G V L G H A F P P G P G	188
CCT CGC TAT TTT GAT GGT CCC TTG GGA GTG CTT GGC CAT GCC TTT CCT CCT GGT CCG GGT	608
L G G D T H F D E D E N W T K D G A G F	208
CTG GGT GGT GAC ACT CAT TTT GAT GAG GAT GAA AAC TGG ACC AAG GAT GGA GCA GGA TTC	668
N L F L V A A H E F G H A L G L S H S N	228
AAC TTG TTT CTT GTG GCT GCT CAT GAA TTT GGT CAT GCA CTG GGC CTC TCT CAC TCC AAT	728
D Q T A L M F P N Y V S L D P R K Y P L	248
GAT CAA ACA GCC TTG ATG TTC CCA AAT TAT GTC TCC CTG GAT CCC AGA AAA TAC CCA CTT	788
S Q D D I N G I Q S I Y G G L P K V P A	268
TCT CAG GAT GAT ATC AAT GGA ATC CAG TCC ATC TAT GGA GGT CTG CCT AAG GTA CCT GCT	848
K P K E P T I P H A C D P D L L T F D A I	288
AAG CCA AAG GAA CCC ACT ATA CCC CAT GCC TGT GAC CCT GAC TTT GAC GCT ATC	908
T T F R R E V M F F K G R H L L W R I Y Y	308
ACA ACT TTC CGC AGA GAA GTA ATG TTC TTT AAA GGC AGG CAC CTA TGG AGG ATC TAT TAT	968

Fig. 15B

D	I	T	D	V	E	F	E	L	I	A	S	F	W	P	S	L	P	A	D	328
GAT	ATC	ACG	GAT	GTT	GAG	TTT	GAA	TTA	ATT	GCT	TCA	TTT	TGG	CCA	TCT	CTG	CCA	GCT	GAT	1028
L	Q	A	A	Y	E	N	P	R	D	K	I	L	V	F	K	D	E	N	F	348
CTG	CAA	GCT	GCA	TAC	GAG	AAC	CCC	AGA	GAT	AAG	ATT	CTG	GTT	TTT	AAA	GAT	GAA	AAC	TTC	1088
W	M	I	R	G	Y	A	V	L	P	D	Y	P	K	S	I	H	T	L	G	368
TGG	ATG	ATC	AGA	GGA	TAT	GCT	GTC	TTG	CCA	GAT	TAT	CCC	AAA	TCC	ATC	CAT	ACA	TTA	GGT	1148
F	P	G	R	V	K	K	I	D	A	A	V	C	D	K	T	T	R	K	T	388
TTT	CCA	GGA	CGT	GTG	AAG	AAA	ATA	GAT	GCA	GCC	GTC	TGT	GAT	AAG	ACC	ACA	AGA	AAA	ACC	1208
Y	F	F	V	G	I	W	C	W	R	F	D	E	M	T	Q	T	M	D	K	408
TAC	TTC	TTT	GTG	GGC	ATT	TGG	TGC	TGG	AGG	TTT	GAT	GAA	ATG	ACC	CAA	ACC	ATG	GAC	AAA	1268
G	F	P	Q	R	V	V	K	H	F	P	G	I	S	I	R	V	D	A	A	428
GGA	TTC	CCG	CAG	AGA	GTG	GTA	AAA	CAC	TTT	CCT	GGA	ATC	AGT	ATC	CGT	GTT	GAT	GCT	GCT	1328
F	Q	Y	K	G	F	F	F	F	S	R	G	S	K	Q	F	E	Y	N	I	448
TTC	CAG	TAC	AAA	GGA	TTC	TTT	TTT	TTC	AGC	CGT	GGA	TCA	AAG	CAA	TTT	GAA	TAC	AAC	ATT	1388
K	T	K	N	I	T	R	I	M	R	T	N	T	W	F	Q	C	K	E	P	468
AAG	ACA	AAG	AAT	ATT	ACC	CGA	ATC	ATG	AGA	ACT	AAT	ACT	TGG	TTT	CAA	TGC	AAA	GAA	CCA	1448

Fig. 15C

K	N	S	S	F	G	F	D	I	N	K	E	K	A	H	S	G	G	I	K	488
AAG	AAC	TCC	TCA	TTT	GGT	TTT	GAT	ATC	AAC	AAG	GAA	AAA	GCA	CAT	TCA	GGA	GGC	ATA	AAG	1508
I	L	Y	H	K	S	L	S	L	F	I	F	G	I	V	H	L	L	K	N	508
ATA	TTG	TAT	CAT	AAG	AGT	TTA	AGC	TTG	TTT	ATT	TTT	GGT	ATT	GTT	CAT	TTG	CTG	AAA	AAC	1568
T	S	I	Y	Q	*															514
ACT	TCT	ATT	TAT	CAA	TAA															1586
ATT	CAT	AGACCT	AAAT	AAACCT	CAACAGG	CTCTTT	TTAAT	ATAAA	ATTCTGCTT	CAAAAT	AGAA	TAAAA	CCATTCTTT	TAAC	1665					
AAC	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA														1684

Fig. 15D

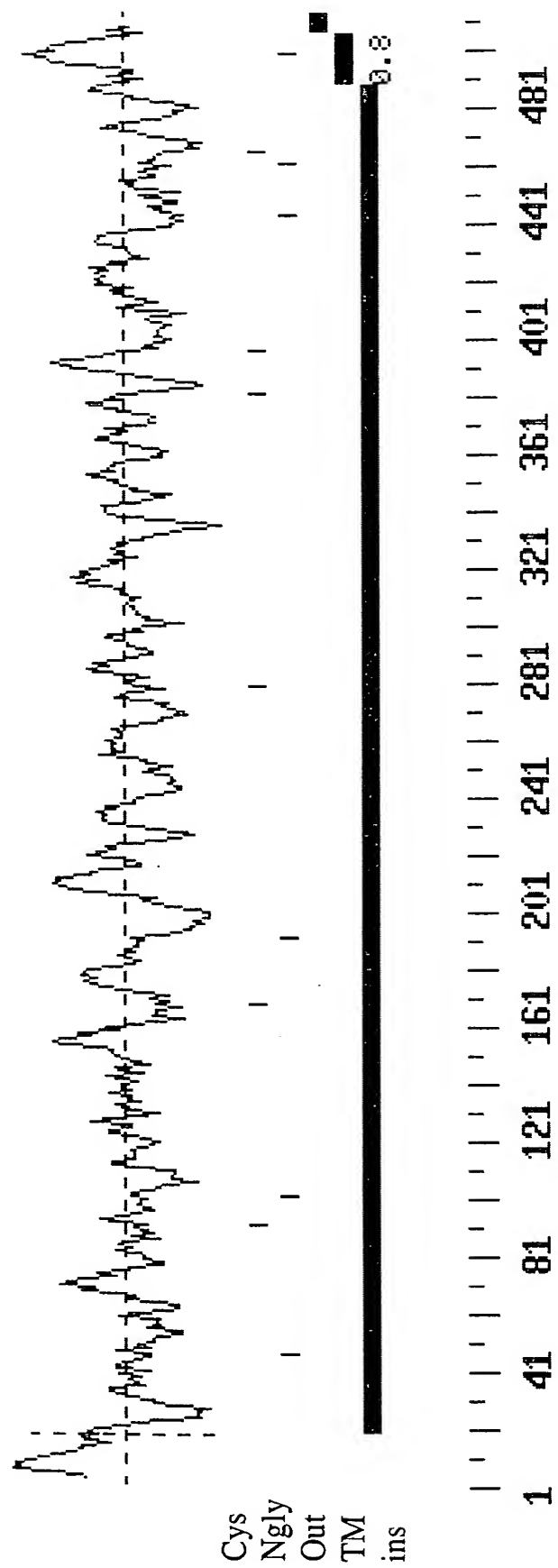


Fig. 15E

A	D	I	M	I	A	F	R	T	G	V	H	G	W	C	P	R	H	F	D	173
GCA	GAT	ATA	ATG	ATA	GCA	TTC	AGG	ACA	GGA	GTC	CAT	GGC	TGG	TGT	CCT	CGT	CAC	TTT	GAT	540
G	P	L	G	V	L	G	H	A	F	P	P	G	L	G	L	G	G	D	T	193
GGT	CCT	CTG	GGA	GTC	CTT	GGC	CAT	GCC	TTT	CCT	CCT	GGT	CTG	GGT	CTA	GGT	GGT	GAC	ACT	600
H	F	D	E	D	E	T	W	I	A	K	D	G	E	G	F	N	L	F	L	213
CAC	TTT	GAC	GAA	GAT	GAA	ACA	TGG	ATA	GCC	AAG	GAT	GGG	GAA	GGG	TTC	AAC	TTG	TTT	CTT	660
V	A	A	H	E	F	G	H	S	L	G	L	S	H	S	N	D	Q	T	A	233
GTG	GCT	GCT	CAT	GAA	TTT	GGT	CAC	TCT	CTG	GGG	CTG	TCC	CAC	TCC	AAT	GAT	CAA	ACA	GCC	720
L	M	F	P	N	Y	I	S	L	D	P	S	K	Y	P	L	S	Q	D	D	253
TTG	ATG	TTC	CCC	AAT	TAC	ATC	TCC	CTG	GAT	CCT	AGC	AAA	TAC	CCA	CTT	TCT	CAG	GAT	GAT	780
I	D	G	I	Q	S	I	Y	G	S	P	P	K	V	T	T	K	P	S	G	273
ATT	GAT	GGG	ATC	CAG	TCC	ATC	TAT	GGA	AGT	CCA	CCT	AAG	GTA	ACC	ACC	AAG	CCA	AGT	GGA	840
N	S	E	P	H	A	C	D	P	T	L	T	F	D	A	I	T	T	F	R	293
AAT	TCT	GAA	CCC	CAC	GCC	TGT	GAC	CCC	ACC	TTG	ACT	TTT	GAT	GCT	ATC	ACT	ACT	TTC	CGC	900
R	E	V	M	F	F	K	G	R												302
AGG	GAA	GTT	ATG	TTC	TTT	AAA	GGC	AGG												927

Fig. 15G

TAAACCTATTCCCTTGACACTCCAGCTTCTTATAAAGATGTTTTTTTTTTTCAAGGATCTCCGGATAAACAGTCTTCTA	1007
CTCAGCTAGAAAGCCAGTTGCTGAGCATGTACCAAGTACATCAGCAAGAGATTCTTCTCAAGAAACAATGTAGAAACAA	1087
TCAAAGAAAACACCCCAAGGCAACCTGCAGCCTCCACACATAAGCACACATGCATTCACATGTATGCCCCACATATGTGA	1167
ACATGTAGGCACACATGCATGCCATACCACAAACCACAACTTAAGACTGAAACATGCTGATGGACACAGGTACCAGGACA	1247
TCATTGATGAAAATATTTTGTGTTTAATGCAGG	1279
H L W R V Y S D I A G A E F E F I D S F	322
CAC TTA TGG AGG GTC TAC TCT GAT ATT GCT GGT GCT GAG TTT GAG TTT ATT GAT TCC TTC	1339
W P S L P A D L Q A A Y E S P R D E L L	342
TGG CCA TCT CTG CCA GCT GAT CTT CAA GCT GCC TAT GAA AGC CCC AGA GAT GAG CTC CTT	1399
V F K D E N F W V I R G Y S V L P G Y P	362
GTT TTT AAA GAT GAG AAT TTC TGG GTC ATC AGG GGA TAT TCT GTC TTC CCC GGT TAC CCC	1459
K S I H T L G F P R R V K K I D A A V C	382
AAA TCC ATC CAC ACA CTC GGA TTT CCA AGA CGT GTG AAG AAA ATT GAT GCA GCC GTC TGT	1519
D H D T R K T F F F V G I W C W R Y D E	402
GAT CAT GAT ACA AGA AAA ACC TTC TTT GTT GGC ATC TGG TGC TGC TGG AGG TAT GAT GAG	1579
M A Q A M D R G F P Q R I I K C F P G I	422
ATG GCA CAA GCA ATG GAC AGA GGA TTC CCA CAG AGG ATA ATA AAG TGC TTC CCA GGA ATT	1639

Fig. 15H

R	L	R	V	D	A	V	F	Q	H	N	G	F	L	Y	F	F	H	G	S	442
CGC	CTC	CGT	GTG	GAT	GCT	GTC	TTC	CAA	CAT	AAT	GGA	TTC	CTC	TAT	TTC	TTC	CAT	GGG	TCG	1699
R	Q	F	E	Y	D	M	K	A	K	N	I	T	Q	V	I	K	T	N	S	462
AGG	CAA	TTT	GAA	TAT	GAC	ATG	AAG	GCG	AAA	AAT	ATC	ACC	CAA	GTG	ATC	AAA	ACC	AAT	TCT	1759
W	F	L	C	N	E	P	L	N	A	S	F	N	V	S	V	K	G	K	A	482
TGG	TTC	CTG	TGT	AAC	GAA	CCA	TTA	AAC	GCA	TCA	TTC	AAT	GTC	AGT	GTC	AAA	GGA	AAA	GCA	1819
N	S	I	G	T	V	I	L	H	H	K	R	L	S	L	L	T	F	S	I	502
AAT	TCA	ATT	GGC	ACA	GTG	ATA	TTA	CAT	CAT	AAA	AGG	TTA	AGC	TTG	CTC	ACT	TTC	AGT	ATT	1879
V	H	V	L	T	K	T	Y	N	*											511
GTT	CAT	GTG	CTG	ACA	AAA	ACA	TAC	AAT	TAA	CAATAAA	TTCCACA	AAATAAA	CCAAA	CAAAATCTTTTAACC						1949
TGA	ACT	CTG	CC	TCAGGA	AGACTCA	AGAGTGG	GAGAGATG	ACCCAGTGGTTA	AGTGCACTGGCTGCTCTTTCAAAGGACCC											2029
AGG	TTTGAT	TTCTCAGT	ACCCACATGG	CAGTCCACAGCTCTCTGTAACTCCAGACCCAGGAAATCTGATGCCCTCTCTGG																2109
CCT	CTGAGG	CAC	TGCACA	AGCATGGTGCATAGACATATACATGCAAGCAACGGCTATATATTAAATAAATGAAAA																2189
AGT	AAAAATAATTGAG	CCCAATTCTTTAGCATCAAGTTCTTACTCTACTATATATCAGCTGGGTAACCAATAAACCAGTTA																		2269
AAG	TATCTGAT	TTCTTAACAGTGAAGTTTAAATATGACAAAAATCTCTCACTTATTTTGAGTCTAAATGATTGC																		2349
AAACTTGG	AAAAATTAAAGCATGTCTTAA	AAAAATAAACATTAAGACAATTCTTAATCCAAAA																		2429
AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	2467

Fig. 15I

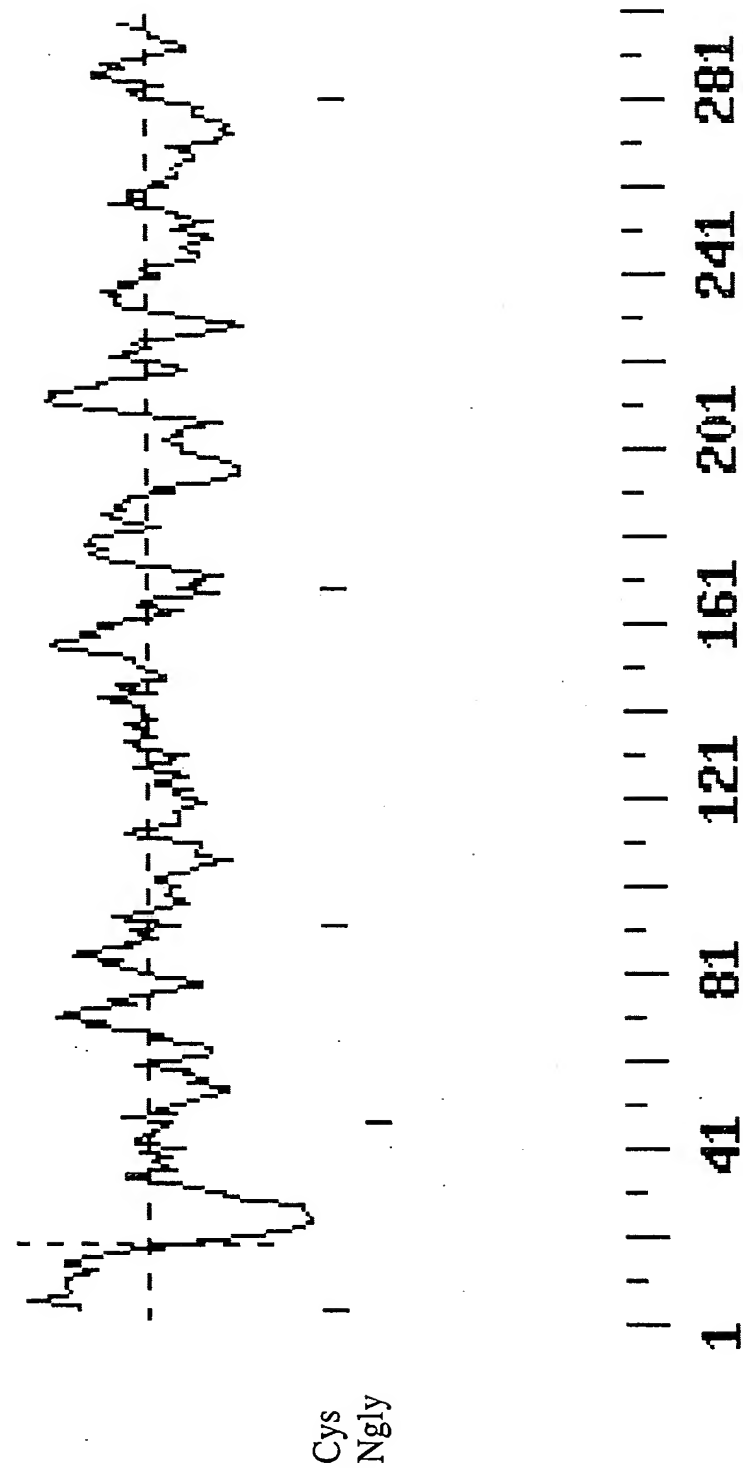


Fig. 15J

human	10	20	30	40	50	60
	MKRLLLFLFFITFSSAFPLVRMTENEENMQAQAYLNQFYSLIEGNHLVQSKNRS	10	20	30	40	50
murine	10	20	30	40	50	60
	10	20	30	40	50	60
human	70	80	90	100	110	120
	70	80	90	100	110	120
murine	70	80	90	100	110	120
	70	80	90	100	110	120
human	140	150	160	170	180	190
	140	150	160	170	180	190
murine	140	150	160	170	180	190
	140	150	160	170	180	190
human	210	220	230	240	250	260
	210	220	230	240	250	260
murine	210	220	230	240	250	260
	210	220	230	240	250	260

Fig. 15K

	280	290	300	310	320	330	340
human	PTIPHACDPDLTFDAIT	TFRRREVMFFKGRHLWRIYYDITDVEFFELIASFWPSLPADLQAAYENPRDKILV					

murine	NSEPHACDPDLTFDAIT	TFRRREVMFFKGRHLWRVYS	DIAGAEFFIDSFWPSPADLQAAYESPRDELLV				
	280	290	300	310	320	330	340
	350	360	370	380	390	400	410
human	FKDENFWMIRGYAVLPDY	PKSIHTLGFPGRVKKIDAAVCDKTT	TRKTYFFVGIWCWRFDEMTQTMDKGFPQ				

murine	FKDENFWIRGYSVLPGY	PKSIHTLGFPRRVKKIDAAVCDHDTRK	TFFVGIWCWRYDEMAQAAMDRGFPQ				
	350	360	370	380	390	400	410
	420	430	440	450	460	470	480
human	RVVKHFPGISIRVDAA	FQYKGFFFSRGSQ	QFEYNIKT	KNITRIMRTNTWFQCKE	PKNSSFGFDINKEKA		

murine	RIIKCFPGIRLRVDA	VFQHNGLYFFHGS	RQFEYDMKAKNITQVIKTNSWFLCNEPLNASFNVS	V-KGKA			
	420	430	440	450	460	470	480
	490	500	510				
human	HSGGIKILYHKSLSL	FIFGIVHLLKNTSIYQ					

murine	NSIGTVILHHKRLSL	LLTFSIVHVLTKTYN					
	490	500	510				

Fig. 15L

[illegible]

Fig. 15M

human	290	300	310	320	330	340	350
	CTCAAAACACCCCTTGAGATCATGAAGACACCCAGGTGTGGGTGCCCTGATGTGGGCCAGTATGGCTACACC						
murine	260	270	280	290	300	310	320
	TTCAGACACACTTGGCGATCATGAAAGTGCCCGAGGTGTGGGTACCCAGATGTGGGGCAATATGGCTACACA						
human	360	370	380	390	400	410	420
	CTCCCTGGGTGGAGAAAATACAACCTCACCTACAGAAATAATAAACTATACTCCGGATATGGCAGAGCTG						
murine	330	340	350	360	370	380	390
	CTCCCTGGGTGGAGAAAATACAGCCTTACATACAGAAATAATGAACCTATACTCCTGATATGACACCCAGCTG						
human	430	440	450	460	470	480	490
	CTGTGGATGAGGCTATCCAAAGAAGGTTTAGAAGTGTGGAGCAAAAGTCACCTCCACTAAAAATTCACCAAGAT						
murine	400	410	420	430	440	450	460
	ATGTGGATGAGGCTATTTCAGAAAGCTCTACAAGTTTGGAGCAAGGTCACCTCCACTGACGTTTACCCAGGAT						
human	500	510	520	530	540	550	560
	TTCAAAGGGGATTGCAGACATCATGATTGCCCTTTAGGACTCGAGTCCCATGGTCCGGTGTCCTCGCTATTTT						
murine	470	480	490	500	510	520	530
	ATCCAAGGGGTTGCAGATATAATGATAGCATTCAGGACAGGAGTCCCATGGCTGGTGTCTCCTCGTCACTTT						

Fig. 15N

human	570	580	590	600	610	620	630
	GATGGTCCCTTGGGAGTGCTTGGCCATGCCTTTCCTCCTGGTCCGGGCTCTGGTGGTGACACTCATTTTG						
murine	540	550	560	570	580	590	600
	GATGGTCCCTCTGGGAGTCCTTGGCCATGCCTTTCCTCCTGGTCTGGGCTAGGTGGTGACACTCACTTTTG						
human	640	650	660	670	680	690	
	ATGAGGATGAAAACTGGA--CCAAGGATGGAGCAGGATTCAACTTGTTCCTTGTGGCTGCTCATGAATT						
murine	610	620	630	640	650	660	670
	ACGAAGATGAACAATGGATAGCCAAAGGATGGGAAGGTTCAACTTGTTCCTTGTGGCTGCTCATGAATT						
human	700	710	720	730	740	750	760
	TGGTCATGCACTGGGGCTCTCTCACTCCAATGATCAAAACAGCCCTTGATGTTCCCAAATTATGTCTCCCTG						
murine	680	690	700	710	720	730	740
	TGGTCACTCTCTGGGGCTGTCCCACCTCCAATGATCAAAACAGCCCTTGATGTTCCCAAATTACATCTCCCTG						
human	770	780	790	800	810	820	830
	GATCCCAGAAAAATACCCACTTTCTCAGGATGATATCAATGGAATCCAGTCCCATCTATGGAGGTCTGCCTA						
murine	750	760	770	780	790	800	810
	GATCCTAGCAAAATACCCACTTTCTCAGGATGATATTGATGGGATCCAGTCCCATCTATGGAAGTCCACCTA						

Fig. 150

```

      840      850      860      870      880      890      900
human  AGGTACCTGCTAAGCCAAAGGAACCCACTATACCCCATGCCTGTGACCCCTGACTTTTGACGCTAT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
murine AGGTAACCAACCAAGCCAAGTGGAATTCCTGAACCCCAACGCTGTGACCCCACTTGACTTTTGATGCTAT
      820      830      840      850      860      870      880

      910      920      930      940
human  CACAACCTTCCGCAGAGAAAGTAATGTTCTTTAAAGGCAGG-----
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
murine CACTACTTTCGCGCAGGGAAGTTATGTTCTTTAAAGGCAGGTAAACCTATTCCCTTGACACTCCAGCTTCT
      890      900      910      920      930      940      950

human  -----

murine TATAAAGATGTTTTTTTTTTTCAAGGATCTCCGGATAAACAGTCTTCTACTCAGCTAGAAAGCCAGTTG
      960      970      980      990      1000      1010      1020

human  -----

murine CTGAGCATGTACCAGTACATCAGCAAGAGATTCTTCTCAAGAAACAATGTAGAAACAATCAAAGAAAA
      1030      1040      1050      1060      1070      1080      1090

```

Fig. 15P

```

950 -----
human -----

murine CACCCAAAGGGCAACCTGCAGCCTCCACACACATAAGCACACATGCATTACACATGTATGCCCCACATATGTGA
1100 1110 1120 1130 1140 1150 1160

human -----

murine ACATGTAGGCACACATGCATGCATACCAACAACCAAACTTAAGACTGAAACATGCTGTATGGACACACAGG
1170 1180 1190 1200 1210 1220 1230

human -----
960 970
-----CACCTATGGAGGATCTATTATGATATCA
::: ::::::::::::::: : ::::: .
murine TACCAGGACATCATTGATGAAATATTTTGTGTTTAATGCAGGCACCTTATGGAGGGTCTACTCTGATATTG
1240 1250 1260 1270 1280 1290 1300

human 980 990 1000 1010 1020 1030 1040
CGGATGTTGAGTTTGAAATTGAATTGCTTCATCTGGCCATCTCTGCCAGCTGATCTGCAAGCTGCATACGA
: ::: ::::::::::::::: ::: ::::::::::::::: ::::::::::::::: ::::::::::::::: :::
murine CTGGTGCTGAGTTTGAGTTTATGATTCCCTTCTGGCCATCTCTGCCAGCTGATCTTCAAGCTGCCCTATGA
1310 1320 1330 1340 1350 1360 1370

```

Fig. 15Q

	1050	1060	1070	1080	1090	1100	1110
human	GAACCCAGAGATAAGATTCTGGTTTTTAAAGATGAAAACTTCTGGATGATCAGAGATATGCTGTCTTG						

murine	AAGCCCCAGAGATGAGCTCCTTGTGTTTTTAAAGATGAGAAATTTCTGGGTCAATCAGGGGATATTCTGTCTTG						
	1380	1390	1400	1410	1420	1430	1440
	1120	1130	1140	1150	1160	1170	1180
human	CCAGATTATCCCAAATCCATCCATACATTAGGTTTTCCAGGACGTGTGAAGAAAAATAGATGCAGCCGTCT						
	:: ::::	:: ::::	:: ::::	:: ::::	:: ::::	:: ::::	:: ::::
murine	CCCGGTTACCCCAAATCCATCCACACACTCGGATTTCCAAAGACGTGTGAAGAAAAATTGATGCAGCCGTCT						
	1450	1460	1470	1480	1490	1500	1510
	1190	1200	1210	1220	1230	1240	1250
human	GTGATAAGACCACACAAGAAAAACCTACTTCTTTGTGGGCATTTGGTGCTGGAGGTTTGATGAAATGACCCA						
	:::: :	:::: ::	:::: ::	:::: ::	:::: ::	:::: ::	:::: ::
murine	GTGATCATGATACACAAGAAAAACCTTCTTTTGTGTCATCTGGTCTGGAGGTATGATGAGATGGCACA						
	1520	1530	1540	1550	1560	1570	1580
	1260	1270	1280	1290	1300	1310	1320
human	AACCATGGACAAAGGATTCCCGCAGAGAGTGGTAAACACTTTCTCTGGAATCAGTATCCCGTTGATGCT						
	:: ::::	:: ::::	:: ::::	:: ::::	:: ::::	:: ::::	:: ::::
murine	AGCAATGGACAGAGGATTCCCCACAGAGGATAATAAAGTGCTTCCCAGGAATTCGCCCTCCCGTGTGGATGCT						
	1590	1600	1610	1620	1630	1640	1650

Fig. 15R

[illegible]

Fig. 15S

human	1670	TAACAACAA-----	
		::::::	
murine		TAGCATCAAGTTCTTACTCCTACTATATATCAGCTGGGTAACCAATAACCAAGTTAAAGTATCTGATTC	2280
	2220	2230 2240 2250 2260 2270	
human		-----	
murine		CTAACAGTGAAGTTTAAATATGACAAAAATCTCTCACTTATTTTGAGTCTAAATTAATGATTTGC	2350
	2290	2300 2310 2320 2330 2340	
human		-----	
murine		TGGAAAAATTAAAGCATGTCCTTAAAAATAAACATTAAAGACAATTCTTAATCCAAAAA	2420
	2360	2370 2380 2390 2400 2410	
human		-----	
	1680	-----AAAAA	
		::::::	
murine		AAAAAAAAAAAAAAAAAAAAAAAAAAAA	2460
	2430	2440 2450	

Fig. 15U

210	M---	KRL	LL	FL	FF	IT	FS	SA	PL	VR	MT	ENE	MQ	LA	QY	LN	QF	YS	LE	IE	GN	HL	VQ	SK	NR	SL	DD	KI	RE	MQ					
	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:						
MMP-8	MF	SL	KT	LP	FL	LL	LV	QI	SK	AF	PV	---	SS	KE	NT	KT	TV	QD	YL	EF	YQ	LP	SN	QY	QSTR	KN	GT	NV	IV	EK	LE	MQ			
	10				20					20				30					40						50				60						
70		80			90				100					110					120						130										
210	AF	FG	LT	VT	GK	LD	SN	TL	EM	KT	PR	CG	VP	DV	GQ	GY	TL	--	PG	WR	KY	NL	TY	RI	IN	YTP	DM	AR	AA	VD	EAI	Q	EGL		
	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:			
MMP-8	RF	FG	LN	VT	GK	PN	EE	TL	DM	KK	PR	CG	VP	DS	GG	FM	LT	PG	NP	PK	WE	RN	LT	YR	IR	NY	TP	QL	SE	AE	VE	RA	IK	DAF	
	70		80			90			100					110					120						130										
140		150			160				170					180					190						200										
210	EV	WS	KV	TP	PL	KFT	KI	SK	GI	AD	IM	IA	FR	TR	VH	GR	CP	RY	FD	GP	LG	VL	GH	AF	PP	GP	GL	GG	DT	HF	DE	DN	WT	KDG	
	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:		
MMP-8	EL	WS	VA	SP	LI	FR	IS	Q	GE	AD	IN	IA	FY	QR	DH	GN	SP	-	FD	GP	NG	IL	AH	AF	Q	PG	Q	IG	IG	DA	HF	DA	EET	WT	NTS
	140		150			160			170					180					190						200										
210		220			230				240					250					260						270										
210	AG	FN	FL	VA	AH	EF	GH	AL	GL	SH	SN	DQ	TAL	MF	PN	YV	SL	DP	PK	YPL	SQ	DD	ING	IQ	SI	YG	GL	PK	VP	AK	PK	EP	TI		
	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:		
MMP-8	AN	YN	FL	VA	AH	EF	GH	SL	GL	AH	SS	DP	GA	LM	YP	NY	AF	RE	TS	NY	SL	PQ	DD	ID	IG	IQ	AI	YG	-	LSS	NP	IQ	PT	GP	ST
	210		220			230			240					250					260						270										

Fig. 15V

[illegible]

Fig. 15W

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10      20      30      40      50      60
210 ATGAAGCGCCCTTCT---GCTTCTGTGTTTTGTTCTTTATATAACATTTTCT-TCTGCAATTTCCCTTAGTCCG
    : : : : : : : : : : : : : : : : : : : : : : : :
MMP-8 ATGTT-CTCCCTGAAGACGCTTCCATTTCTGCTCTTACTC-CATGTGCAGATTTCCAAGGCCCTT--TCCT
    10      20      30      40      50      60

70      80      90      100     110     120     130
210 GATGACGGAAATGAAGAAATA-TGCAACTGGCTCAGGCATATCTCAACCAGTTCTACTCTCTTGAAAT
    : : : : : : : : : : : : : : : : : : : : : : : :
MMP-8 G-TATCTTCTAAAGAGAAATAACAAAACTGT-TCAGGACTACCTGGAAAAAGTTCTAC-CAATTACCAA
    70      80      90      100     110     120     130

140     150     160     170     180     190     200
210 AGAAG-GGAATCATCTTGTTCAAAGCAAGAATAG---GAGTCTCATAGATGACAAAAATTCGGGAAATGCA
    . : : : : : : : : : : : : : : : : : : : : : : :
MMP-8 GCAACCAGTATCAG--TCTACAAGG-AAGAATGGCACTAATGTGATCGTTGAAAAGCTTAAAGAAATGCA
    140     150     160     170     180     190     200

210     220     230     240     250     260     270
210 AGCATTTTTTGGATTGACAGTGAAGTGGGAAAACCTGGACTCAAACACCCCTTGAGATCATGAAGACACCCAGG
    . : : : : : : : : : : : : : : : : : : : : : : :
MMP-8 GCGATTTTTTGGGTTGAATGTGACGGGGAAGCCAAATGAGGAAACTCTGGACATGATGAAAAAGCCTCGC
    210     220     230     240     250     260     270

```

Fig. 15X-1

210	TGTGGGTGCCTGA-TGTGG-GCCAGTATGGCTACACCC-----TCCCTGGGTGGAGAAAAATACAACCTCA	280	290	300	310	320	330	340
MMP-8	TTTTTTTTTTTTTTTTTTTATGTTAACCCAGGAAACCCCAAGTGGGAAACGCACATAACTTGA	280	290	300	310	320	330	340
210	CCTACAGAAATAAACTATACTCCGGGATATGGCACGAGCTGCTGTGGATGAGGCTATCCAAAGAAGGTTT	340	350	360	370	380	390	400
MMP-8	CTTCAAGGATTCGAAACTATACCCACACAGCTGTACAGAGGCTGAGGTAGAAAGAGCTATCAAGGATGCCCTT	350	360	370	380	390	400	410
210	AGAAGTGTGGAGCAAAGTCACCTCCACTAAATAATTCACCAAGATTTCAAAGGGGATTGCAGACATCATGATT	410	420	430	440	450	460	470
MMP-8	TGAACCTCTGGAGTGTTCATCACCTCTCATCTTCACACAGGATCTCACAGGAGAGGCAGATATCAACATT	420	430	440	450	460	470	480
210	GCCTTTAGGACTCGAGTCCATGGTCGGTGTCCCTCGCTATTTTGATGGTCCCTTGGGAGTGCTTGGCCATG	480	490	500	510	520	530	540
MMP-8	GCTTTTACCAAAGAGATCACGGTGACAATTCCTC-CA--TTTGATGAGACCCCAATGGAATCCTTGCTCATG	490	500	510	520	530	540	

Fig. 15X-2


```

550      560      570      580      590      600      610
210 CCTTCCCTCGGTCCGGGTCTGGGTGGTGACACTCATTTTGATGAGGATGAAAACTGGACCAAGGATGG
MMP-8 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
550      560      570      580      590      600      610
CCTTTCAGCCAGGCCAAGGTATTGGAGGAGAGATGCTCATTTTGATGCCGAAAGAAACATGGACCAACACCTC

620      630      640      650      660      670      680
210 AGCAGGATTCAACTTGTTTCTTGTTGGCTGCTCATGAATTTGGTCATGCACCTGGGGCTCTCTCACTCCAAT
MMP-8 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
620      630      640      650      660      670      680
CGCAAATTACAACCTTGTTTCTTGTTGCTGCTCATGAATTTGGCCCATTCCTTTGGGGCTCGCTCACTCCTCT

690      700      710      720      730      740      750
210 GATCAAACAGCCTTGATGTTCCCAAATTATGTCTCCCTGGATCCCAGAAAAATACCCACTTTCCTCAGGATG
MMP-8 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
690      700      710      720      730      740      750
GACCCCTGGTGCCTTGATGTATCCCAACTATGCTTTCAGGGAAACCAGCAACTACTCACTCCCTCAAGATG

760      770      780      790      800      810      820
210 ATATCAATGGAATCCAGTCCATCTATGGAGGTCTGCCCTAAGGTACCTGCTAAGCCAAAGGAACCCACTAT
MMP-8 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
760      770      780      790      800      810      820
ACATCGATGGCATTTCAGGCCATCTATGGA---CTTCAAGCAACCCCTATCCAACCTACTGGACCAAGCAC

```

Fig. 15X-3

	830	840	850	860	870	880	890
210	ACCCCATGCCCTGTGACCCCTGACTTTGACGCTATCACAACTTTCGCAGAGAAGTAATGTTCTTT						
MMP-8	ACCCAACCCTGTGACCCCAGTTTGACATTTGATGCTATCACCACACTCCGTGGAGAAAATACTTTTCTTT						
	830	840	850	860	870	880	890
	900	910	920	930	940	950	960
210	AAAGGCAGGCACCTATGGAGGAT-CTATTATGATATCACGGATGTTGAGTTTGAATTAATTGCTTCATTTC						
MMP-8	AAAGACAGGTACTTCTGGAGAAGGCATCCCTCAGCTACAAGA-GTCGAAATGAATTTTATTCTCTCTATTTC						
	900	910	920	930	940	950	960
	970	980	990	1000	1010	1020	1030
210	TGGCCATCTCTGCCAGCTGATCTGCAAGCTGCATACGAGAACCC--CAGAGATAAGATTCTGGTTTTTA						
MMP-8	TGGCCATCCCTTCCAACCTGGTATACAGGCTGCTTATGAAGATTTTGACAGAGACCTCATTTTCCCTATTTA						
	970	980	990	1000	1010	1020	1030
	1040	1050	1060	1070	1080	1090	
210	AAGATGAAAACTTCTGGATGATCAGAGGATATGCTGTCTTGCCAGATTATCCCCAAATCCATC-CATACAT						
MMP-8	AAGGCAACCAATACTGGGCTCTGAGTGGCTATGATATTCTGCAAGGTTATCCCCAAGGATATATCAAAC-T						
	1040	1050	1060	1070	1080	1090	1100

Fig. 15X-4

```

1100      1110      1120      1130      1140      1150      1160
210 TAGGTTTTCAGGACGTGTGAAGAAAAATAGATGCAGCCGTCTGTGATAAGACCACAAGAAAAACCTACTT
    ::: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
MMP-8 ATGGCTTCCCCAGCAGCGTCCAAGCAATTGACGCAGC-----TGTTTCTACAGAAGTAAAAACATACTT
1110      1120      1130      1140      1150      1160

1170      1180      1190      1200      1210      1220      1230
210 CTTTGTGGGCATTTGGTGTGGAGGTTTGATGAAATGACCCAAACCATGGACAAAGGATTCCCCGCAGAGA
    ::: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
MMP-8 CTTTGTAATGACCCAATTCTGGAGATATGAT-----AACCAAAGACAATT-----CATGGAGC
1170      1180      1190      1200      1210

1240      1250      1260      1270      1280      1290      1300
210 GTGGTAAACACTTTCCCTGGAATCAGTATCCGTTGTGATGCTGCTTTCAGTACAAAGGATTCTTCTTTT
    ::: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
MMP-8 CAGGT-----TATCCCAAAGCA-TATC-----AGGTGC--CTTTCAGGAATAGAGAGTAAA-----
1220      1230      1240      1250      1260

1310      1320      1330      1340      1350      1360      1370
210 TCAGCCGTGGATCAAAGCAATTGAAATACAACATTAAGACAAAGAATATTACCCGAATCATGAGAACTAA
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
MMP-8 -----GTTGAT----GCAGTTT---TCCAGCA-----AGAACATTC-----TTC-----
1270      1280      1290      1300

```

Fig. 15X-5

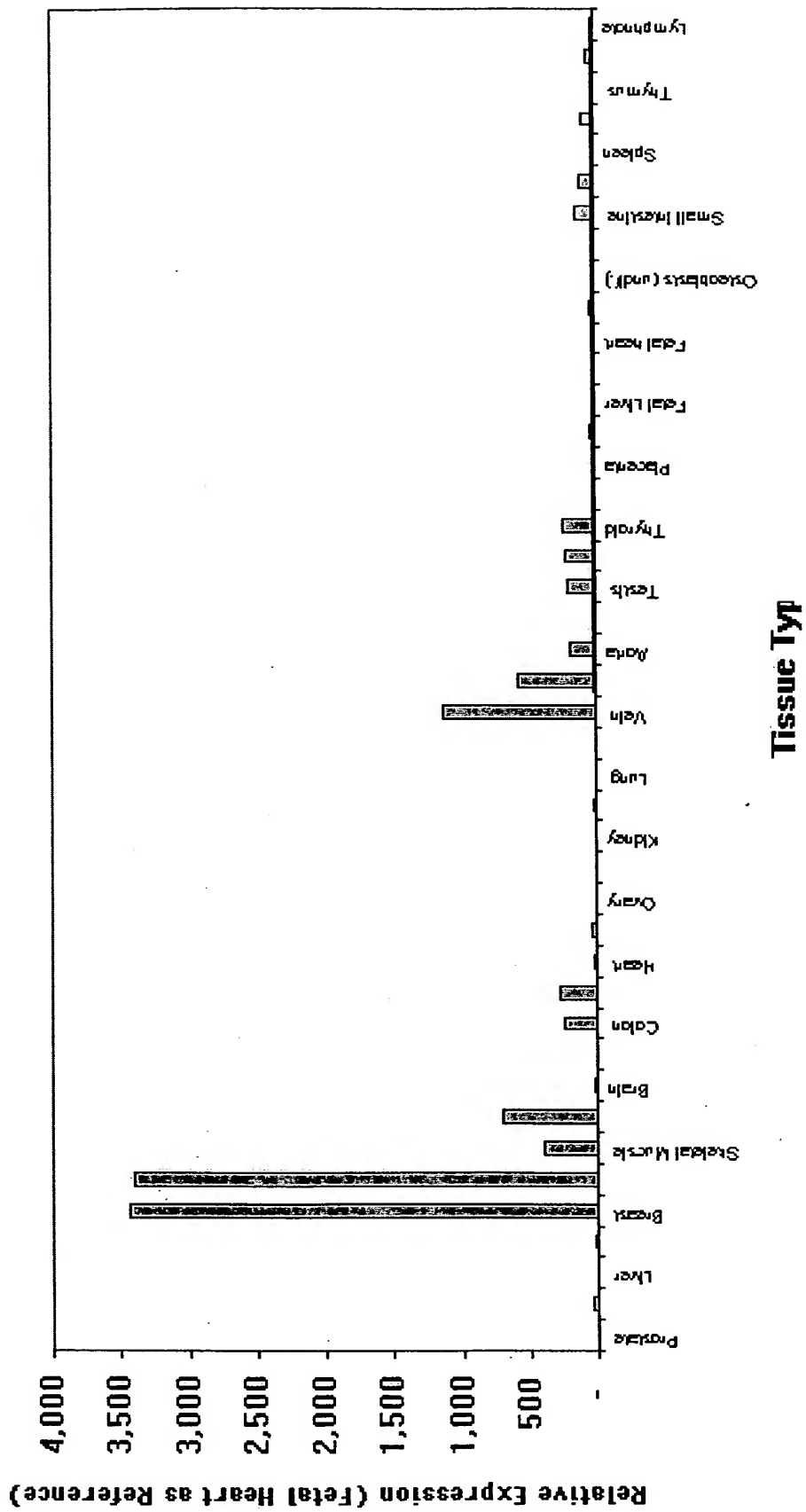


Fig. 15Y

S	H	N	Q	L	R	E	V	S	V	S	A	F	T	T	H	S	Q	G	R	158
AGC	CAC	AAC	CAG	CTC	CGG	GAG	GTC	TCA	GTG	TCT	GCC	TTC	ACG	ACG	CAC	AGT	CAG	GGC	CGG	559
A	L	H	V	D	L	S	H	N	L	I	H	R	L	V	P	H	P	T	R	178
GCA	CTA	CAC	GTG	GAC	CTC	TCC	CAC	AAC	CTC	ATT	CAC	CGC	CTC	GTG	CCC	CAC	CCC	ACG	AGG	619
A	G	L	P	A	P	T	I	Q	S	L	N	L	A	W	N	R	L	H	A	198
GCC	GGC	CTG	CCT	GCG	CCC	ACC	ATT	CAG	AGC	CTG	AAC	CTG	GCC	TGG	AAC	CGG	CTC	CAT	GCC	679
V	P	N	L	R	D	L	P	L	R	Y	L	S	L	D	G	N	P	L	A	218
GTG	CCC	AAC	CTC	CGA	GAC	TTG	CCC	CTG	CGC	TAC	CTG	AGC	CTG	GAT	GGG	AAC	CCT	CTA	GCT	739
V	I	G	P	G	A	F	A	G	L	G	G	L	T	H	L	S	L	A	S	238
GTC	ATT	GGT	CCG	GGT	GCC	TTC	GCG	GGG	CTG	GGA	GGC	CTT	ACA	CAC	CTG	TCT	CTG	GCC	AGC	799
L	Q	R	L	P	E	L	A	P	S	G	F	R	E	L	P	G	L	Q	V	258
CTG	CAG	AGG	CTC	CCT	GAG	CTG	GCG	CCC	AGT	GGC	TTC	CGT	GAG	CTA	CCG	GGC	CTG	CAG	GTC	859
L	D	L	S	G	N	P	K	L	N	W	A	G	A	E	V	F	S	G	L	278
CTG	GAC	CTG	TCG	GGC	AAC	CCC	AAG	CTT	AAC	TGG	GCA	GGA	GCT	GAG	GTG	TTT	TCA	GGC	CTG	919
S	S	L	Q	E	L	D	L	S	G	T	N	L	V	P	L	P	E	A	L	298
AGC	TCC	CTG	CAG	GAG	CTG	GAC	CTT	TCG	GGC	ACC	AAC	CTG	GTG	CCC	CTG	CCT	GAG	GCG	CTG	979

Fig. 16B

L	L	H	L	L	P	A	L	Q	S	V	S	V	G	Q	D	V	R	C	R	R	318									
CTC	CTC	CAC	CTC	CCG	GCA	CTG	CAG	AGC	AGC	GTC	AGC	GTG	GGC	CAG	GAT	GTG	CGG	TGC	CGG	CGC	1039									
L	V	R	E	G	T	Y	P	P	R	R	P	G	S	S	P	K	V	A	L	H	338									
CTG	GTG	CGG	GAG	GGC	ACC	TAC	CCC	CGG	AGG	CCT	GGC	GGC	TCC	AGC	CCC	AAG	GTG	GCC	CTG	CAC	1099									
C	V	D	T	R	E	S	A	A	R	G	P	T	I	L	*						354									
TGC	GTA	GAC	ACC	CGG	GAA	TCT	GCT	GCC	AGG	GGC	CCC	ACC	ATC	TTG	TGA						1147									
CAA	ATG	TG	TG	GGC	CCAC	ATA	CAG	ACT	GTG	TCT	GGG	CTG	CCCT	CAG	GTCCC	GAG	TAA	CTT	ATG	TCA	ATGTG	1226								
CCA	AC	AC	AGG	GGG	GAG	CCCG	AGC	CTAT	GTG	GCA	GGT	CAC	CAC	AGG	ATT	TGT	GGC	CTAG	GAG	AGG	CTTT	TGG	ACCT	1305						
GGG	AG	CC	AC	ACT	AGG	AGCA	AA	GTCT	CAC	CCCT	TTT	GTCT	TAC	GTCT	TCC	CA	AA	CCAT	GAG	CAG	AGG	ACTT	CG	ATGC	1384					
CAA	AC	CAG	ACT	CGG	TCCC	CTG	CTT	CCCT	TCC	CACT	TAT	CCCC	CA	AGT	CCCT	TCC	CTC	ATG	CCCT	GAT	GCCT	GGC	CGC	CTG	1463					
AC	CC	GCA	AT	GGG	CAG	AGG	TGG	GAC	CCCT	GTG	CTG	CAG	GGC	AG	TT	CAG	GTCC	ACT	GGC	TG	AGT	GTCC	CCCT	TGG	1542					
G	CC	AT	GG	CC	CAG	TCA	CT	AG	CCCT	TTT	CT	TAA	CA	TAG	CCCT	TTT	TG	CCAT	GAG	CCAT	GAG	CC	CCG	CTT	1621					
CAT	CC	TTT	CT	AT	TCC	CTA	GA	ACCT	TAA	TGG	TAG	AA	GA	AT	CA	AGT	CC	AC	CCCT	TCT	CA	TGT	GAC	AGAT	1700					
GGG	AA	ACT	GAG	CCCT	TG	AG	AA	GGG	CTAA	TCT	AGT	TCC	TG	CGG	CAGT	GG	CA	TG	ACT	GAG	CAC	AGC	CTC	CT	1779					
G	CC	TCC	AG	CCCG	ACCA	ATG	CA	CTT	TCT	TG	CTC	CTA	ATA	AG	CCCC	AC	CCCT	CC	CGC	CTG	GGC	TCCC	CTT	GCT	TGC	1858				
C	CT	TG	CC	TG	TCCC	AT	TAG	CAC	AGG	AGT	AGC	AGC	AGC	AGC	CA	AGT	GG	ACT	C	TG	GGC	CTC	TG	1937						
A	CC	AG	CT	GTG	CGG	CA	TGG	CTA	AGT	CA	CT	TG	CCCT	TTC	GAG	CCCT	CT	G	AAG	CT	TAG	GC	CA	AT	TGGT	TCC	AGC	CTAGC	2016	
C	AGT	TT	CT	CA	CCCT	TGGG	TCCCC	AGC	AT	CC	AG	CTG	GAA	AC	TAC	CC	AT	TTT	CCCC	CT	GAG	CA	TCC	CT	CTAG	ATG	2095			
CTG	CCCC	AA	GG	AGT	TG	CTG	CAG	CT	CTG	GAG	CCCT	CA	TCT	G	G	AT	CT	CA	AGG	GGC	CTC	CTG	GAT	T	CAGT	CCCC	CACT	2174		
GG	CC	CT	GAG	CAC	GAC	CCCT	TCT	TAC	CCCT	CC	AG	GA	AT	G	CC	G	T	G	AA	AG	GAG	ACA	AGG	T	CTG	CCCC	GAC	CCAT	GTCTATG	2253

Fig. 16C

CTCTACCCAGGCAGCATCTCAGCTTCCGAACCCCTGGGCTGTTTCCCTTAGTCCTTCATTTATATAAAAGTTGTTGCCCTT 2332
TTTAACGGAGTGCACTTTCAACCGGCTCCCTACCCCTGCTGCGCGGATGGAGACATGTCAATTTGTAAAGCAGA 2411
AAAAGGTGCATTTGTTCACTTTTGTAAATATTGTCCTGGCCCTGTGTTGGGTGTTGGGGAAGCTGGGCATCAGTGGC 2490
CACATGGGCATCAGGGGCTGGCCCCACAGGACCCCCACAGGGCAGTGAGCTCTGTCTTCCCCCACCTGCCCTAGCCCCATC 2569
ATCTATCTAACCGGTCCTTGATTTAATAAACACTATATAAAAGTTATAAAAAA 2628

Fig. 16D

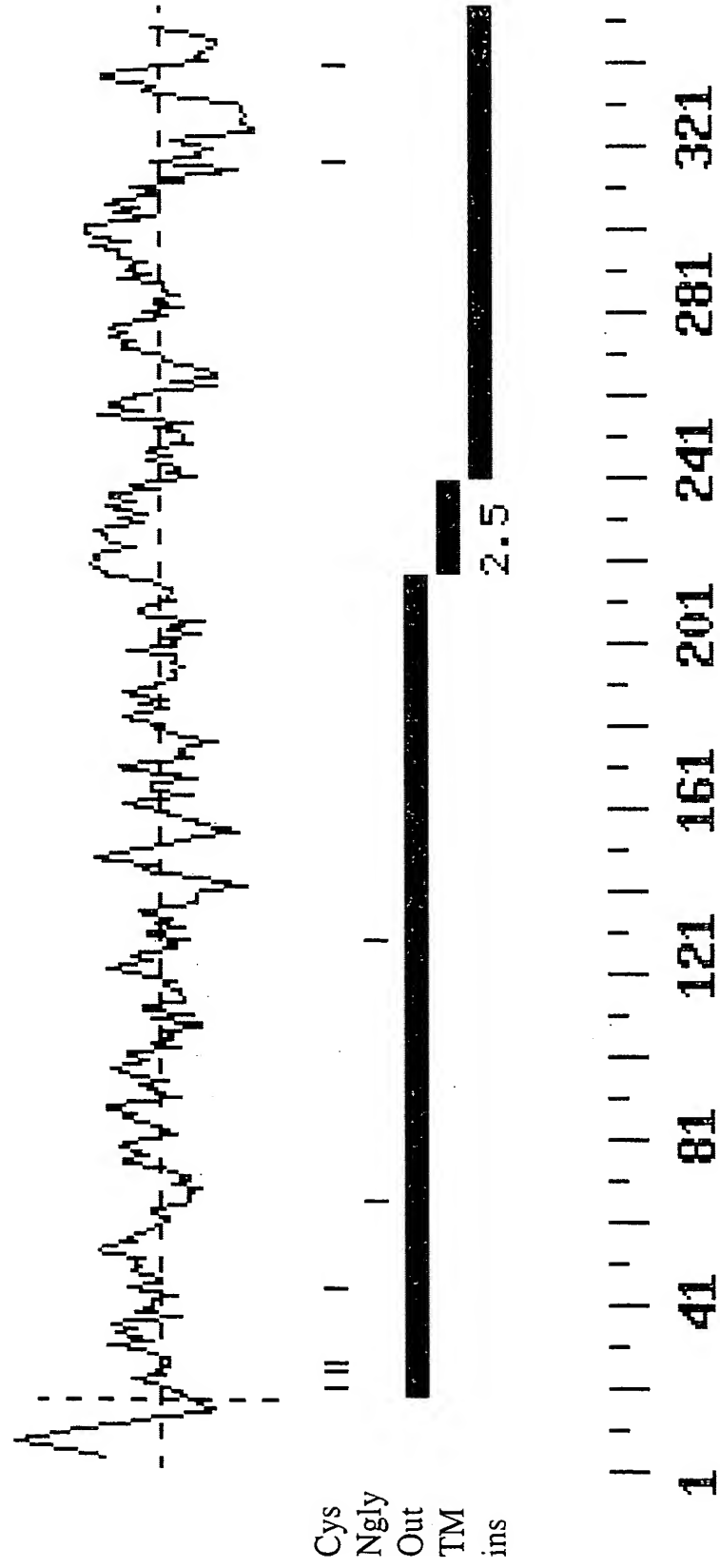


Fig. 16E

GTCGACCCACGCGTCCGCCCCGGCC	TA	GCGCGCGGT	CGCGCGAGCCGAGCCGAGCGGAGCCGGGAGCCCTC	79																
TGGAATCACCCGGGTGCTGTTCC	TGAGGT	CAAGGTGACAGGGGCGGTG	TGATGGCGCAGTTTGACACTGAAT	158																
ACCAGGCCCTAGAGGCCTCCTAT	AGTAT	GCACCCCGAGGAGGACCTGTT	GGTGACGTCGCCGAGGGAGCAA	237																
GTCACCTTGGCACCATATTGAA	AACCTTGACCTCTCTCTCGAGTT	ATAATCTGCACCAAGAAATGGCTTCACA	316																	
M	L	I	G	E	I	F	E	L	M	Q	F	L	F	V	V	A	F	T	19	
TGT	ATG	CTC	ATC	GGG	GAG	ATC	TTT	GAG	CTC	ATG	CAG	TTC	CTC	TTT	GTG	GTT	GCC	TTC	ACT	376
T	F	L	V	S	C	V	D	Y	D	I	L	F	A	N	K	M	V	N	H	39
ACC	TTC	CTG	GTC	AGC	TGC	GTG	GAC	TAT	GAC	ATC	CTA	TTT	GCC	AAC	AAG	ATG	GTG	AAC	CAC	436
S	L	H	P	T	E	P	V	K	V	T	L	P	D	A	F	L	P	A	Q	59
AGT	CTT	CAC	CCT	ACT	GAA	CCC	GTC	AAG	GTC	ACT	CTG	CCA	GAC	GCC	TTT	TTG	CCT	GCT	CAA	496
V	C	S	A	R	I	Q	E	N	G	S	L	I	T	I	L	V	I	A	G	79
GTC	TGT	AGT	GCC	AGG	ATT	CAG	GAA	AAT	GGC	TCC	CTT	ATC	ACC	ATC	CTG	GTC	ATT	GCT	GGT	556
V	F	W	I	H	R	L	I	K	F	I	Y	N	I	C	C	Y	W	E	I	99
GTC	TTC	TGG	ATC	CAC	CGG	CTT	ATC	AAG	TTC	ATC	TAT	AAC	ATT	TGC	TGC	TAC	TGG	GAG	ATC	616
H	S	F	Y	L	H	A	L	R	I	P	M	S	A	L	P	Y	C	T	W	119
CAC	TCC	TTC	TAC	CTG	CAC	GCT	CTG	CGC	ATC	CCT	ATG	TCT	GCC	CTT	CCG	TAT	TGC	ACG	TGG	676

Fig. 17A

Q	E	V	Q	A	R	I	V	Q	T	Q	K	E	H	Q	I	C	I	H	K	139
CAA	GAA	GTG	CAG	GCC	CGG	ATC	ATC	GTG	CAG	ACG	AAG	GAG	CAC	CAG	ATC	TGC	ATC	CAC	AAA	736
R	E	L	T	E	L	D	I	Y	H	R	I	L	R	F	Q	N	Y	M	V	159
CGT	GAG	CTG	ACA	GAA	CTG	GAC	ATC	TAC	CAC	CAC	ATC	CTC	CGT	TTC	CAG	AAC	TAC	ATG	GTG	796
A	L	V	N	K	S	L	L	P	L	R	F	R	L	P	G	L	G	E	A	179
GCA	CTG	GTT	AAC	AAA	TCC	CTC	CTG	CCT	CTG	CGC	TTC	CGC	CTG	CCT	GGC	CTC	GGG	GAA	GCT	856
V	F	F	T	R	G	L	K	Y	N	F	E	L	I	L	F	W	G	P	G	199
GTC	TTC	TTC	ACC	CGT	GGT	CTC	AAG	TAC	AAC	TTT	GAG	CTG	ATC	CTC	TTC	TGG	GGA	CCT	GGC	916
S	L	F	L	N	E	W	S	L	K	A	E	Y	K	R	G	G	Q	R	L	219
TCT	CTG	TTT	CTC	AAT	GAA	TGG	AGC	CTC	AAG	GCC	GAG	TAC	AAA	CGT	GGG	GGG	CAA	CGG	CTA	976
E	L	A	Q	R	L	S	N	R	I	L	W	I	G	I	A	N	F	L	L	239
GAG	CTG	GCC	CAG	CGC	CTC	AGC	AAC	CGC	ATC	CTG	TGG	ATT	GGC	ATC	GCT	AAC	TTC	CTG	CTG	1036
C	P	L	I	L	I	W	Q	I	L	Y	A	F	F	S	Y	A	E	V	L	259
TGC	CCC	CTC	ATC	CTC	ATA	TGG	CAA	ATC	CTC	TAT	GCC	TTC	TTC	AGC	TAT	GCT	GAG	GTG	CTG	1096
K	R	E	P	G	A	L	G	A	R	C	W	S	L	Y	G	R	C	Y	L	279
AAG	CGG	GAG	CCG	GGG	GCC	CTG	GGA	GCA	CGC	TGC	TGG	TCA	CTC	TAT	GGC	CGC	TGC	TAC	CTC	1156

Fig. 17B

R	H	F	N	E	L	E	H	E	L	Q	S	R	L	N	R	G	Y	K	P	299
CGC	CAC	TTC	AAC	GAG	CTG	GAG	CAC	GAG	CTG	CAG	TCC	CGC	CTC	AAC	CGT	GGC	TAC	AAG	CCC	1216
A	S	K	Y	M	N	C	F	L	S	P	L	L	T	L	L	A	K	N	G	319
GCC	TCC	AAG	TAC	ATG	AAT	TGC	TTC	TTG	TCA	CCT	CTT	TTG	ACA	CTG	CTG	GCC	AAG	AAT	GGA	1276
A	F	F	A	G	S	I	L	A	V	L	I	A	L	T	I	Y	D	E	D	339
GCC	TTC	TTC	GCT	GGC	TCC	ATC	CTG	GCT	GTG	CTT	ATT	GCC	CTC	ACC	ATT	TAT	GAC	GAA	GAT	1336
V	L	A	V	E	H	V	L	T	T	V	T	L	L	G	V	T	V	T	V	359
GTG	TTG	GCT	GTG	GAA	CAT	GTG	CTG	ACC	ACC	GTC	ACA	CTC	CTG	CTG	GTC	ACC	GTG	ACC	GTG	1396
C	R	S	F	I	P	D	Q	H	M	V	F	C	P	E	Q	L	L	R	V	379
TGC	AGG	TCC	TTT	ATC	CCG	GAC	CAG	CAC	ATG	GTG	TTC	TGC	CCT	GAG	CAG	CTG	CTC	CGC	GTG	1456
I	L	A	H	I	H	Y	M	P	D	H	W	Q	G	N	A	H	R	S	Q	399
ATC	CTC	GCT	CAC	ATC	CAC	TAC	ATG	CCT	GAC	CAC	TGG	CAG	GGT	AAT	GCC	CAC	CGC	TCG	CAG	1516
T	R	D	E	F	A	Q	L	F	Q	Y	K	A	V	F	I	L	E	E	L	419
ACC	CGG	GAC	GAG	TTT	GCC	CAG	CTC	TTC	CAG	TAC	AAG	GCA	GTG	TTC	ATT	TTG	GAA	GAG	TTG	1576
L	S	P	I	V	T	P	L	I	L	I	F	C	L	R	P	R	A	L	E	439
CTG	AGC	CCC	ATT	GTC	ACA	CCC	CTC	ATC	CTC	ATC	TTC	TGC	CTG	CGC	CCA	CGG	GCC	CTG	GAG	1636

Fig. 17C

I	I	D	F	F	TTC	TTC	CGA	AAC	TTC	ACC	GTG	GAG	GTC	GTT	GGT	GTG	GGA	GAT	ACC	TGC	TCC	S	459
ATT	ATA	GAC	TTC	TTC	CGA	AAC	TTC	ACC	GTG	GAG	GTC	GTT	GGT	GTG	GGA	GAT	ACC	TGC	TCC				1696
F	A	Q	M	D	GAT	GAT	GTT	CGC	CAG	CAT	GGT	CAT	CCC	CAG	TGG	CTA	TCT	GCT	GGG	CAG	ACA	T	479
TTT	GCT	CAG	ATG	ATG	GAT	GAT	GTT	CGC	CAG	CAT	GGT	CAT	CCC	CAG	TGG	CTA	TCT	GCT	GGG	CAG	ACA		1756
E	A	S	V	Y	TAC	TAC	CAG	CAA	GCT	GAG	GAT	GGA	AAG	ACA	GAG	TTG	TCA	CTC	ATG	CAC	TTT	F	499
GAG	GCC	TCA	GTG	TAC	TAC	CAG	CAA	GCT	GAG	GAT	GGA	AAG	ACA	GAG	TTG	TCA	CTC	ATG	CAC	TTT		1816	
A	I	T	N	P	G	G	W	Q	P	P	P	R	E	S	T	A	F	L	G	F	L	519	
GCC	ATC	ACC	AAC	CCT	GGC	GGC	TGG	CAG	CCA	CCA	CGT	GAG	AGC	ACA	GCC	TTC	CTA	GGC	TTC	CTC		1876	
K	E	Q	V	Q	CAG	CGG	GAT	GGA	GCA	GCT	GCT	AGC	AGC	CTC	GCC	CAA	GGG	GGT	CTG	CTC	P	539	
AAG	GAG	CAG	GTT	CAG	CGG	GAT	GGA	GCA	GCT	GCT	AGC	AGC	CTC	GCC	CAA	GGG	GGT	CTG	CTC	CCT		1936	
E	N	A	L	F	T	ACG	TCT	ATC	CAG	TCC	TTA	CAA	TCT	GAG	TCT	GAG	CCC	CTG	AGC	CTT	L	559	
GAA	AAT	GCC	CTC	TTT	ACG	TCT	ATC	CAG	TCC	TTA	CAA	TCT	GAG	TCT	GAG	CCC	CTG	AGC	CTT		1996		
I	A	N	V	V	A	G	S	S	S	C	R	G	P	P	L	P	R	D	L	Q		579	
ATC	GCA	AAT	GTG	GTA	GCT	GGC	TCA	TCC	TCC	TGC	CGG	GGC	CCT	CCA	CTG	CCC	AGA	GAC	CTG	CAG		2056	
G	S	R	H	R	A	E	V	A	S	A	L	R	S	F	S	P	L	Q	P			599	
GGC	TCC	AGG	CAC	AGG	GCT	GAA	GTC	GCC	TCT	GCC	CTG	CGC	TCC	TTC	TCC	CCG	CTG	CAA	CCC			2116	

Fig. 17D

G	Q	A	P	T	G	R	A	H	S	T	M	T	G	S	G	V	D	A	R	619
GGG	CAG	GCG	CCC	ACA	GGC	CGG	GCT	CAC	AGC	ACC	ATG	ACA	GGC	TCT	GGG	GTG	GAT	GCC	AGG	2176
T	A	S	S	G	S	S	V	W	E	G	Q	L	Q	S	L	V	L	S	E	639
ACA	GCC	AGC	TCC	GGG	AGC	AGC	GTG	TGG	GAA	GGA	CAG	CTG	CAG	AGC	CTG	GTG	CTG	TCA	GAA	2236
Y	A	S	T	E	M	S	L	H	A	L	Y	M	H	Q	L	H	K	Q	Q	659
TAT	GCA	TCC	ACA	GAG	ATG	AGC	CTG	CAT	GCC	CTC	TAT	ATG	CAC	CAG	CTC	CAC	AAG	CAG	CAG	2296
A	Q	A	E	P	E	R	H	V	W	H	R	R	E	S	D	E	S	G	E	679
GCC	CAG	GCT	GAA	CCT	GAG	CGG	CAT	GTA	TGG	CAC	CGC	CGG	GAG	AGT	GAT	GAG	AGT	GGA	GAA	2356
S	A	P	D	E	G	G	E	G	A	R	A	P	Q	S	I	P	R	S	A	699
AGC	GCC	CCT	GAT	GAA	GGG	GGA	GAG	GGC	GCC	CGG	GCC	CCC	CAG	TCT	ATC	CCT	CGC	TCT	GCT	2416
S	Y	P	C	A	A	P	R	P	G	A	P	E	T	T	A	L	H	G	G	719
AGC	TAT	CCC	TGT	GCA	GCA	CCC	CGG	CCT	GGA	GCT	CCT	GAG	ACC	ACC	GCC	CTG	CAT	GGG	GGC	2476
F	Q	R	R	Y	G	G	I	T	D	P	G	T	V	P	R	V	P	S	H	739
TTC	CAG	AGG	CGC	TAC	GGT	GGC	ATC	ACA	GAT	CCT	GGC	ACA	GTG	CCC	AGG	GTT	CCC	TCT	CAT	2536
F	S	R	L	P	L	G	G	W	A	E	D	G	Q	S	A	S	R	H	P	759
TTC	TCT	CGG	CTG	CCT	CTT	GGA	GGG	TGG	GCA	GAA	GAT	GGG	CAG	TCG	GCA	TCA	AGG	CAC	CCT	2596

Fig. 17E

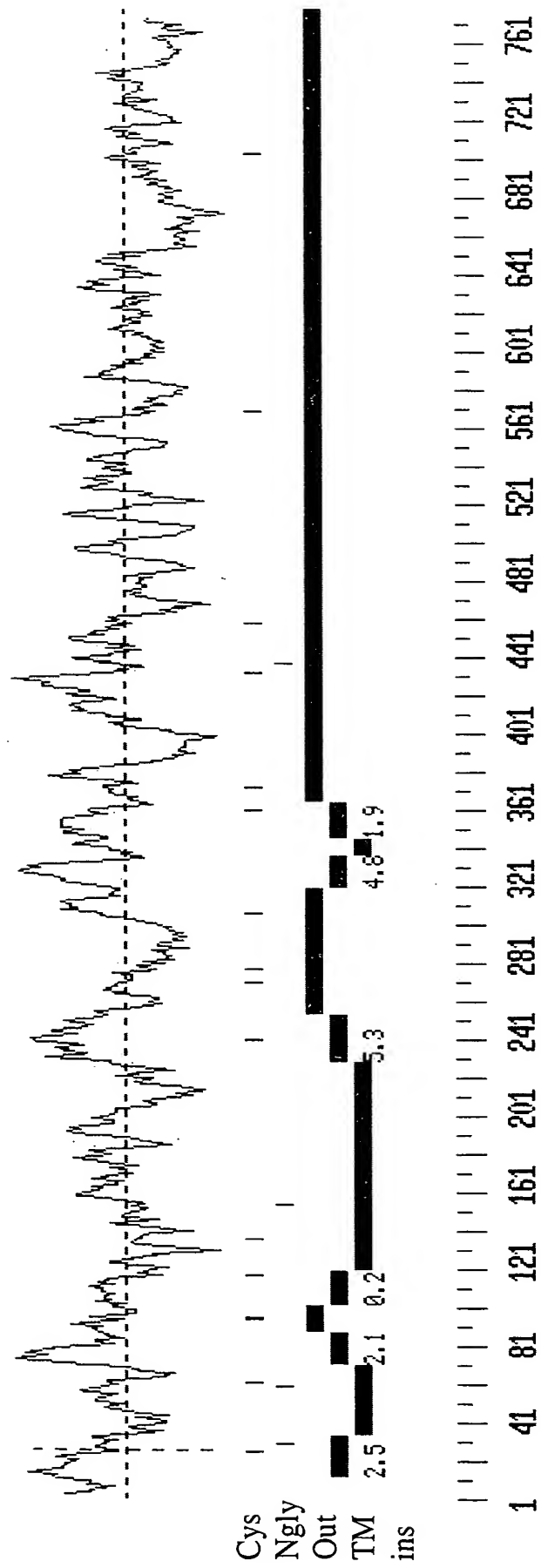


Fig. 17G

CCCCGCCCTAGCGCCGCGGTCTCGCGCCGAGCCGAGCCGAGCCGAGCCGCGGAGCCCTCTGGAATCACCCGGGTCG	79
<div style="text-align: center;">M A Q F D T E Y Q</div>	
CTGTTCTGAGGTGGTCAAGGTGGACAGGGCGGTGGTG ATG GCG CAG TTT GAC ACT GAA TAC CAG	9 146
R L E A S Y S D S P P G E D L L V H V	29
CGC CTA GAG GCC TCC TAT AGT GAT TCA CCC CCA GGG GAG GAG GAC CTG TTG GTG CAC GTC	206
A E G S K S P W H H I E N L D L F F S R	49
GCC GAG GGG AGC AAG TCA CCT TGG CAC CAT ATT GAA AAC CTT GAC CTC TTC TTC TCT CGA	266
V Y N L H Q K N G F T C M L I G E I F E	69
GTT TAT AAT CTG CAC CAG AAG AAT GGC TTC ACA TGT ATG CTC ATC GGG GAG ATC TTT GAG	326
L M Q F L F V V A F T T F L V S C V D Y	89
CTC ATG CAG TTC CTC TTT GTG GTT GCC TTC ACT ACC TTC CTG GTC AGC TGC GTG GAC TAT	386
D I L F A N K M V N H S L H P T E P V K	109
GAC ATC CTA TTT GCC AAC AAG ATG GTG AAC CAC AGT CTT CAC CCT ACT GAA CCC GTC AAG	446
V T L P D A F L P A Q V C S A R I Q E N	129
GTC ACT CTG CCA GAC GCC TTT TTG CCT GCT CAA GTC TGT AGT GCC AGG ATT CAG GAA AAT	506

Fig. 17H

G	S	L	I	T	I	L	V	I	A	G	V	F	W	I	H	R	L	I	K	149
GGC	TCC	CTT	ATC	ACC	ATC	CTG	GTC	ATT	GCT	GGT	GTC	TTC	TGG	ATC	CAC	CGG	CTT	ATC	AAG	566
F	I	Y	N	I	C	C	Y	W	E	I	H	S	F	Y	L	H	A	L	R	169
TTC	ATC	TAT	AAC	ATT	TGC	TGC	TAC	TGG	GAG	ATC	CAC	TCC	TTC	TAC	CTG	CAC	GCT	CTG	CGC	626
I	P	M	S	A	L	P	Y	C	T	W	Q	E	V	Q	A	R	I	V	Q	189
ATC	CCT	ATG	TCT	GCC	CTT	CCG	TAT	TGC	ACG	TGG	CAA	GAA	GTC	CAG	GCC	CGG	ATC	GTG	CAG	686
T	Q	K	E	H	Q	I	C	I	H	K	R	E	L	T	E	L	D	I	Y	209
ACG	CAG	AAG	GAG	CAC	CAG	ATC	TGC	ATC	CAC	AAA	CGT	GAG	CTG	ACA	GAA	CTG	GAC	ATC	TAC	746
H	R	I	L	R	F	Q	N	Y	M	V	A	L	V	N	K	S	L	L	P	229
CAC	CGC	ATC	CTC	CGT	TTC	CAG	AAC	TAC	ATG	GTG	GCA	CTG	GTT	AAC	AAA	TCC	CTC	CTG	CCT	806
L	R	F	R	L	P	G	L	G	E	A	V	F	F	T	R	G	L	K	Y	249
CTG	CGC	TTC	CGC	CTG	CCT	GGC	CTC	GGG	GAA	GCT	GTC	TTC	TTC	ACC	CGT	GGT	CTC	AAG	TAC	866
N	F	E	L	I	L	F	W	G	P	G	S	L	F	L	N	E	W	S	L	269
AAC	TTT	GAG	CTG	ATC	CTC	TTC	TGG	GGA	CCT	GGC	TCT	CTG	TTT	CTC	AAT	GAA	TGG	AGC	CTC	926
K	A	E	Y	K	R	G	G	Q	R	L	E	L	A	Q	R	L	S	N	R	289
AAG	GCC	GAG	TAC	AAA	CGT	GGG	GGG	CAA	CGG	CTA	GAG	CTG	GCC	CAG	CGC	CTC	AGC	AAC	CGC	986

Fig. 17I

I	L	W	I	G	I	A	N	F	L	L	C	P	L	I	L	I	W	Q	I	309
ATC	CTG	TGG	ATT	GGC	ATC	GCT	AAC	TTC	CTG	CTG	TGC	CCC	CTC	ATC	CTC	ATA	TGG	CAA	ATC	1046
L	Y	A	F	F	S	Y	A	E	V	L	K	R	E	P	G	A	L	G	A	329
CTC	TAT	GCC	TTC	TTC	AGC	TAT	GCT	GAG	GTG	CTG	AAG	CGG	GAG	CCG	GGG	GCC	CTG	GGA	GCA	1106
R	C	W	S	L	Y	G	R	C	Y	L	R	H	F	N	E	L	E	H	E	349
CGC	TGC	TGG	TCA	CTC	TAT	GGC	CGC	TGC	TAC	CTC	CGC	CAC	TTC	AAC	GAG	CTG	GAG	CAC	GAG	1166
L	Q	S	R	L	N	R	G	Y	K	P	A	S	K	Y	M	N	C	F	L	369
CTG	CAG	TCC	CGC	CTC	AAC	CGT	GGC	TAC	AAG	CCC	GCC	TCC	AAG	TAC	ATG	AAT	TGC	TTC	TTG	1226
S	P	L	L	T	L	L	A	K	N	G	A	F	F	A	G	S	I	L	A	389
TCA	CCT	CTT	TTG	ACA	CTG	CTG	GCC	AAG	AAT	GGA	GCC	TTC	TTC	GCT	GGC	TCC	ATC	CTG	GCT	1286
V	L	I	A	L	T	I	Y	D	E	D	V	L	A	V	E	H	V	L	T	409
GTG	CTT	ATT	GCC	CTC	ACC	ATT	TAT	GAC	GAA	GAT	GTG	TTG	GCT	GTG	GAA	CAT	GTG	CTG	ACC	1346
T	V	T	L	L	G	V	T	V	T	V	C	R	S	F	I	P	D	Q	H	429
ACC	GTC	ACA	CTC	CTG	GGG	GTC	ACC	GTG	ACC	GTG	TGC	AGG	TCC	TTT	ATC	CCG	GAC	CAG	CAC	1406
M	V	F	C	P	E	Q	L	L	R	V	I	L	A	H	I	H	Y	M	P	449
ATG	GTG	TTC	TGC	CCT	GAG	CAG	CTG	CTC	CGC	GTG	ATC	CTC	GCT	CAC	ATC	CAC	TAC	ATG	CCT	1466

Fig. 17J

D	H	W	Q	G	N	A	H	R	S	Q	T	R	D	E	F	A	Q	L	F	469
GAC	CAC	TGG	CAG	GGT	AAT	GCC	CAC	CGC	TCG	CAG	ACC	CGG	GAC	GAG	TTT	GCC	CAG	CTC	TTC	1526
Q	Y	K	A	V	F	I	L	E	E	L	L	S	P	I	V	T	P	L	I	489
CAG	TAC	AAG	GCA	GTG	TTC	ATT	TTG	GAA	GAG	TTG	CTG	AGC	CCC	ATT	GTC	ACA	CCC	CTC	ATC	1586
L	I	F	C	L	R	P	R	A	L	E	I	I	D	F	F	R	N	F	T	509
CTC	ATC	TTC	TGC	CTG	CGC	CCA	CGG	GCC	CTG	GAG	ATT	ATA	GAC	TTC	TTC	CGA	AAC	TTC	ACC	1646
V	E	V	V	G	V	G	D	T	C	S	F	A	Q	M	D	V	R	Q	H	529
GTG	GAG	GTC	GTT	GGT	GTG	GGA	GAT	ACC	TGC	TCC	TTT	GCT	CAG	ATG	GAT	GTT	CGC	CAG	CAT	1706
G	H	P	Q	W	L	S	A	G	Q	T	E	A	S	V	Y	Q	Q	A	E	549
GGT	CAT	CCC	CAG	TGG	CTA	TCT	GCT	GGG	CAG	ACA	GAG	GCC	TCA	GTG	TAC	CAG	CAA	GCT	GAG	1766
D	G	K	T	E	L	S	L	M	H	F	A	I	T	N	P	G	W	Q	P	569
GAT	GGA	AAG	ACA	GAG	TTG	TCA	CTC	ATG	CAC	TTT	GCC	ATC	ACC	AAC	CCT	GGC	TGG	CAG	CCA	1826
P	R	E	S	T	A	F	L	G	F	L	K	E	Q	V	Q	R	D	G	A	589
CCA	CGT	GAG	AGC	ACA	GCC	TTC	CTA	GGC	TTC	CTC	AAG	GAG	CAG	GTT	CAG	CGG	GAT	GGA	GCA	1886
A	A	S	L	A	Q	G	G	L	L	P	E	N	A	L	F	T	S	I	Q	609
GCT	GCT	AGC	CTC	GCC	CAA	GGG	GGT	CTG	CTC	CCT	GAA	AAT	GCC	CTC	TTT	ACG	TCT	ATC	CAG	1946

Fig. 17K

S	L	Q	S	E	S	E	P	L	S	L	I	A	N	V	V	A	G	S	S	629
TCC	TTA	CAA	TCT	GAG	TCT	GAG	CCC	CTG	AGC	CTT	ATC	GCA	AAT	GTG	GTA	GCT	GGC	TCA	TCC	2006
C	R	G	P	P	L	P	R	D	L	Q	G	S	R	R	A	H	S	T	M	649
TGC	CGG	GGC	CCT	CCA	CTG	CCC	AGA	GAC	CTG	CAG	GGC	TCC	AGG	CGG	GCT	CAC	AGC	ACC	ATG	2066
T	G	S	G	V	D	A	R	T	A	S	S	G	S	S	V	W	E	G	Q	669
ACA	GGC	TCT	GGG	GTG	GAT	GCC	AGG	ACA	GCC	AGC	TCC	GGG	AGC	AGC	GTG	TGG	GAA	GGA	CAG	2126
L	Q	S	L	V	L	S	E	Y	A	S	T	E	M	S	L	H	A	L	Y	689
CTG	CAG	AGC	CTG	GTG	CTG	TCA	GAA	TAT	GCA	TCC	ACA	GAG	ATG	AGC	CTG	CAT	GCC	CTC	TAT	2186
M	H	Q	L	H	K	Q	Q	A	Q	A	E	P	E	R	H	V	W	H	R	709
ATG	CAC	CAG	CTC	CAC	AAG	CAG	CAG	GCC	CAG	GCT	GAA	CCT	GAG	CGG	CAT	GTA	TGG	CAC	CGC	2246
R	E	S	D	E	S	G	E	S	A	P	D	E	G	G	E	G	A	R	A	729
CGG	GAG	AGT	GAT	GAG	AGT	GGA	GAA	AGC	GCC	CCT	GAT	GAA	GGG	GGA	GAG	GGC	GCC	CGG	GCC	2306
P	Q	S	I	P	R	S	A	S	Y	P	C	A	A	P	R	P	G	A	P	749
CCC	CAG	TCT	ATC	CCT	CGC	TCT	GCT	AGC	TAT	CCC	TGT	GCA	GCA	CCC	CGG	CCT	GGA	GCT	CCT	2366
E	T	T	A	L	H	G	G	F	Q	R	R	Y	G	G	I	T	D	P	G	769
GAG	ACC	ACC	GCC	CTG	CAT	GGG	GGC	TTC	CAG	AGG	CGC	TAC	GGT	GGC	ATC	ACA	GAT	CCT	GGC	2426

Fig. 17L

T	V	P	P	R	V	P	S	H	F	S	R	L	P	L	G	G	W	A	E	D	789
ACA	GTG	CCC	AGG	GTT	CCC	TCT	CAT	TTC	TCT	CGG	CTG	CCT	CTT	GGA	GGG	TGG	GCA	GAA	GAT	2486	
G	Q	S	A	S	R	H	P	P	E	P	V	P	E	E	G	S	E	D	E	L	809
GGG	CAG	TCG	GCA	TCA	AGG	CAC	CCT	GAG	CCC	GAG	CCC	GAA	GAG	GGC	TCG	GAG	GAT	GAG	CTA	2546	
P	P	Q	V	H	K	V	*													817	
CCC	CCT	CAG	GTG	CAC	AAG	GTA	TAG													2570	
ACA	AGG	CTG	AGC	AGG	TTT	CTG	TGG	CCC	AGG	ATG	GAG	CC	CGG	CTG	CCC	ATG	CCC	GTG	CTG	2649	
CTC	CTG	AGT	GT	TCC	CTG	GGC	CCC	ACG	GTG	TGG	TGT	TTG	TGT	CTG	TG	CTG	GGC	CAAG	GAG	2728	
TTG	CCAC	AGC	CCC	CAG	GAG	AGG	AAT	TTG	GGC	CTAG	GAAC	CCG	AGG	CAC	ACG	GACT	CTAG	CCCT	ATC	2807	
TTG	GCT	CAG	AGT	GTG	TG	CTAG	AAACT	GGT	CCCC	AGC	CCAG	CCCA	GTACT	GGC	ACCT	TTAC	ACCT	ACCC	CTG	2886	
CCC	AG	GGG	CTG	CCC	ACG	ATAG	AAG	CTGCC	AAG	CAAC	CTGT	GCC	AAC	TGT	GAG	TGG	GAG	GTG	GGC	2965	
CCCT	CA	ACCC	CTG	CA	ACC	TTCC	CTAG	CCCC	CTCA	ATAG	ATG	AGG	TCAG	GGCT	GTG	CCCT	TAC	CTAC	CCG	3044	
TCG	CCC	AGT	GC	AGC	CGG	CTC	AC	CTC	TC	CGG	TTCT	TG	CAC	ATC	AC	TG	GTG	CTG	CTG	3123	
GT	CGC	TTG	CTC	CG	TTCC	GG	CTTT	TG	CGT	TTAG	GGT	GA	AG	AC	CC	TAG	CGT	CC	AG	3202	
ATTT	TG	AC	TA	AAA	AGA	AGT	TTT	CTA	AAAT	TG	TAG	GAG	CAG	GAT	GGA	AA	TACT	TTG	CTC	3281	
TGG	CCCC	CC	AG	GAG	ACT	GAG	GT	CTC	TGG	CCC	TC	ATG	CTG	CTT	AT	CGT	AC	CCCC	ATC	3360	
CCG	GCT	GG	AGG	TG	AC	CTT	GG	CTGT	GTAC	GTCC	AG	CA	AA	AG	AG	CTC	TG	CCCC	GC	3439	
ATGA	AGG	CGG	AT	GC	CTC	GG	CTTT	TGG	GCTG	CTG	CA	TG	CTG	GAG	CTG	CTC	CTAC	TCT	GT	3518	
CAC	CC	AG	CTG	TG	TC	CGG	CTTT	TGG	GAG	AGT	GTGA	ATT	CG	CTG	CCCC	GA	ACT	CG	AG	3597	
ACAG	CT	TG	ATA	AC	CTT	AA	TAA	AA	AGG	AGT	TTG	AC	CA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	3674	

Fig. 17M

GCTGGAGCGGAGCGCAGGCAATGCTCAGCCCTGGATGCTAGAGGGCTGGAGAGACGACCGCTGGAGACCG	79
ACCGCGTGGGAAGACCTAGGGGGTGGTGGGAAGCAGACAGGAGAACACTCGAAATCAAGCGCTTTACAGATTA	158
TTTTATTTTGTATAGAGAACACGTAGCGACTCCGAAGATCAGCCCCA ATG AAC ATG TCA GTG TTG ACT TTA	229
Q E Y E F E K Q F N E N E A I Q W M Q E	28
CAA GAA TAT GAA TTC GAA AAG CAG TTC AAC GAG AAT GAA GCC ATC CAA TGG ATG CAG GAA	289
N W K K S F L F S A L Y A A F I F G G R	48
AAC TGG AAG AAA TCT TTC CTG TTT TCT GCT TAT GCT GCC TTT ATA TTC GGT GGT CGG	349
H L M N K R A K F E L R K P L V L W S L	68
CAC CTA ATG AAT AAA CGA GCA AAG TTT GAA CTG AGG AAG CCA TTA GTG CTC TGG TCT CTG	409
T L A V F S I F G A L R T G A Y M V Y I	88
ACC CTT GCA GTC TTC AGT ATA TTC GGT GCT CTT CGA ACT GGT GCT TAT ATG GTG TAC ATT	469
L M T K G L K Q S V C D Q G F Y N G P V	108
TTG ATG ACC AAA GGC CTG AAG CAG TCA GTT TGT GAC CAG GGT TTT TAC AAT GGA CCT GTC	529
S K F W A Y A F V L S K A P E L G D T I	128
AGC AAA TTC TGG GCT TAT GCA TTT GTG CTA AGC AAA GCA CCC GAA CTA GGA GAT ACA ATA	589

Fig. 18A

F	I	I	L	R	K	Q	K	L	I	F	L	H	Y	H	H	I	T	V	148
TTC	ATT	ATT	CTG	AGG	AAG	CAG	AAG	CTG	ATC	TTC	CTG	CAC	TGG	TAT	CAC	ATC	ACT	GTG	649
L	L	Y	S	W	Y	S	Y	K	D	M	V	A	G	G	W	F	M	T	168
CTC	CTG	TAC	TCT	TGG	TAC	TCC	TAC	TAC	AAA	GAC	ATG	GCC	GGA	GGA	GTT	TTC	ATG	ACT	709
M	N	Y	G	V	H	A	V	M	Y	S	Y	Y	A	L	R	A	A	G	188
ATG	AAC	TAT	GGC	GTG	CAC	GCC	GTG	ATG	TAC	TCT	TAC	TAT	GCC	TTG	CGG	GCA	GGT	TTC	769
R	V	S	R	K	F	A	M	F	I	T	L	S	Q	I	T	Q	M	L	208
CGA	GTC	TCC	CGG	AAG	TTT	GCC	ATG	TTC	ATC	ACC	TTG	TCC	CAG	ATC	ACT	CAG	ATG	CTG	829
G	C	V	V	N	Y	L	V	F	C	W	M	Q	H	D	Q	C	H	S	228
GGC	TGT	GTG	GTT	AAC	TAC	CTG	GTC	TTC	TGC	TGG	ATG	CAG	CAT	GAC	CAG	TGT	CAC	TCT	889
F	Q	N	I	F	W	S	S	L	M	Y	L	S	Y	L	V	L	F	C	248
TTT	CAG	AAC	ATC	TTC	TGG	TCC	TCA	CTC	ATG	TAC	CTC	AGC	TAC	CTT	GTG	CTC	TTC	TGC	949
F	F	F	E	A	Y	I	G	K	M	R	K	T	T	K	A	E	*		266
TTC	TTC	TTT	GAG	GCC	TAC	ATC	GGC	AAA	ATG	AGG	AAA	ACA	ACG	AAA	GCT	GAA	TAG		1003
TGTTGGA	ACTGAGG	AAAGCC	ATAGCTCAGG	GTCA	TCAAG	AAAAA	TAA	TAGAC	AAAAA	ATGGC	ACAAAGGA	ATC	ATC	ATC	ATC	ATC	ATC	ATC	1082
ACGTGGT	GCGCTAA	AAACAAA	CAAAACATGAG	CAAAACATGAG	CAAAACATGAG	CAAAACATGAG	CAAAACATGAG	CAAAACATGAG	CAAAACATGAG	CAAAACATGAG	CAAAACATGAG	CAAAACATGAG	CAAAACATGAG	CAAAACATGAG	CAAAACATGAG	CAAAACATGAG	CAAAACATGAG	CAAAACATGAG	1161

Fig. 18B

CCCAGTAAGTTTATGATCCCTTTTAGGGTGAGGACTCACTGAGTGCACCTCCATCTCCAAGCAGCTGCTGCTGGAAGACCC 1240
 CATCCCTCTTTTATCTATCAACTCTAGGACAAAGGAGAAACAAGCAAGCCAGAACGAGAGAGACTAATCAAAAGGCAA 1319
 ACAAGGCTATTAAACACATAGGAAAAAATGTATTTACTAAGTGTACATTTCTCTAAGATGAAAAGATTTTACTCTAGA 1398
 AACTGTGCGAGCAACAACACACACAATCCCTTTCTAACTTATGGACACTAAACTGGAGCCAAATAGAAAAAGACAAAAATGA 1477
 AAGAGACACAGGGTGATATCTAGAACGATAATGCTTTTGCAGAAACTAAAGCCCTTTTAAAGAAATGCCAGCTGCTGTA 1556
 GACCCCATGAGAAAAAGATGTCTTAATCATCTTATGAAAAACAGATGTAAACAACATAATTTCAAACCTCACTCTTCA 1635
 CTGCATAGCCTCAGGCTAGTGAGTTTGCCAAAACCAAGGGGTGAATACTTCCCCAAGATTTCTCCTGGGAGGATGGA 1714
 AACAGTGCAGCCAGGTCCTCAGGGGAGCTCCATCCAGAGCATTTCTGTAGATTGAACTGTAATTTCTACTCTTAA 1793
 GTGAGATATGAAGCATTAATCCCTTTTGTTCAGTTGCCCGGGCTTTTGAAACAGAAAGATAATACAGAAATTGAAAAAGAT 1872
 AAACACTCAACCAACAATGTGAAAAACGGGTTCTGTAGTATTTGTAAAAAGGCCCGGCCAGGACCACTGTGAGCTGGA 1951
 AAAGGGAGAAAGGCAGTGGGAAAAGAGGTGAGCCGAAGATCAATTCGACAGACAGACGGTGTGTATGCCCTCCCTGTT 2030
 TGACTTCACACACACTCAATACTTTCCAAATGAAACCCACAGTATAGCGCATATTTTCGATATTTTGTGTAATTCCAA 2109
 AAGGAAATCACAGGGCTGTTTCGAAATATTGGGGAACACTGTGTTTCTGCATCATCTGCATTTGCTCCCCAAGCAATGT 2188
 AGAGGTGTTTAAAGGGCCCTCTGCTGGCTGAGTGGCAATACTACAACAACCTCAAGGCAAGTTTGGCTGAAAAACAGTT 2267
 GACAACAAGGGCCCCCATACACTTATCCCTCAAAATTTTAAGTGATATGAAATACTTGTCAATGCTTTGGCCAAATCAG 2346
 AAGATATTCAATCCCTGCTTCAAGTCAGCTTCAGAAATGTTTAAAGGGACTTTAGCTCTGGAACCTCAAAATCAATTTAT 2425
 TAAAGAGCCATATTCTTTAAAAAAAAGCTGGATAATAATTCCTGTAAATATTTTCAGTCCCTTACAAGCCAAATACATG 2504
 TGTCAATGTTTCTAGTATTTCAAAGAAAGCAATATGTAAAGTTGTTCAATGTGACATAATAGTATTAATAATTGGTTAAG 2583
 TAGCTTAATGATTAGGCAAACTAGATGAAAAGATTAGGGGCTTCCACACTGCATAGATTACACGCACATAGCCACGCAT 2662
 ACACACACAGACACACAGATGTGGGTACACTGAACTTCAAAGCCCAAATGAATAGAAACACATTTTCTGGCTAGCAGA 2741
 AAAAAACAACAAAACCTGTGTTTCTCTTCTTCTGCTTTGAGAGTGTACAGTAAAAGGATTTTTCGAAATTAATTTTA 2820
 TATTATTTTAGCTTTAATTGTGCTGCTGTTCAATGAAACAGAGCTGCTCTGCTTTTCTGTCAAGATGGCAAGGCTTTT 2899
 TCAGCATCTCGTTTATGTGTGGAATTTAAAAAGAAATAAAGTTTATTCCATTCTGTGTGAAAAAATAAAAAA 2978
 AAAAAAATAAAA 2989

Fig. 18C

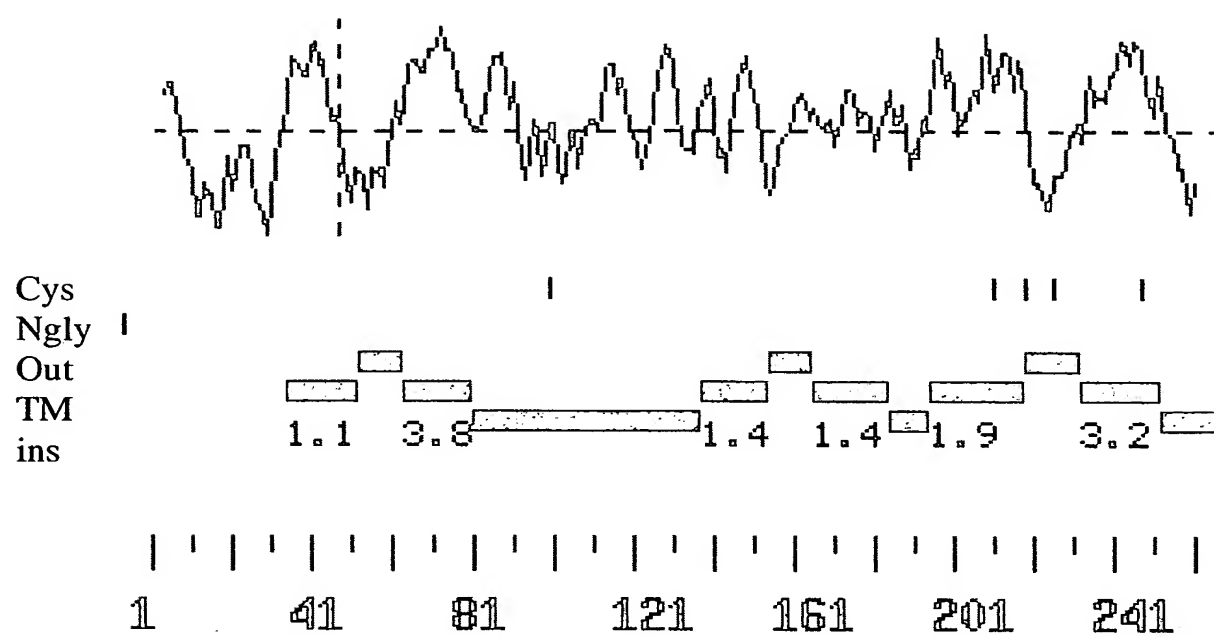


Fig. 18D

L	K	Q	S	V	C	D	Q	S	F	Y	N	G	P	V	S	K	F	W	19	
GC	CTG	AAG	CAG	TCA	GTT	TGT	GAC	CAG	AGT	TTT	TAC	AAT	GGA	CCT	GTC	AGC	AAA	TTC	TGG	59
A	Y	A	F	V	L	S	K	A	P	E	L	G	D	T	I	F	I	I	L	39
GCT	TAT	GCA	TTT	GTG	CTC	AGC	AAA	GCA	CCC	GAA	CTA	GGT	GAC	ACG	ATA	TTC	ATC	ATT	CTG	119
R	K	Q	K	L	I	F	L	H	W	Y	H	H	I	T	V	L	L	Y	S	59
AGG	AAA	CAG	AAA	CTG	ATC	TTT	CTG	CAC	TGG	TAC	CAC	CAC	ATC	ACT	GTG	CTC	CTG	TAC	TCC	179
W	Y	S	Y	K	D	M	V	A	G	G	G	W	F	M	T	M	N	Y	G	79
TGG	TAC	TCC	TAC	AAA	GAC	ATG	GTC	GCT	GGG	GGT	GGT	TGG	TTC	ATG	ACT	ATG	AAC	TAT	GGC	239
V	H	A	V	M	Y	S	Y	Y	A	L	R	A	A	G	F	R	V	S	R	99
GTG	CAT	GCC	GTC	ATG	TAC	TCT	TAC	TAC	GCC	TTG	CGG	GCT	GCG	GGT	TTC	CGA	GTC	TCC	CGG	299
K	F	A	M	F	I	T	L	S	Q	I	T	Q	M	L	M	G	C	V	I	119
AAG	TTT	GCC	ATG	TTT	ATC	ACC	TTG	TCC	CAG	ATC	ACT	CAG	ATG	CTG	ATG	GGC	TGT	GTC	ATT	359
N	Y	L	V	F	N	W	M	Q	H	D	N	D	Q	C	Y	S	H	F	Q	139
AAC	TAC	CTG	GTC	TTT	AAC	TGG	ATG	CAG	CAT	GAC	AAC	GAC	CAG	TGC	TAC	TCC	CAC	TTT	CAG	419
N	I	F	W	S	S	L	M	Y	L	S	Y	L	V	L	F	C	H	F	F	159
AAC	ATC	TTT	TGG	TCC	TCG	CTC	ATG	TAC	CTC	AGC	TAC	CTT	GTG	CTC	TTC	TGC	CAT	TTC	TTC	479

Fig. 18E

F	E	A	Y	I	G	K	V	K	K	A	T	K	A	E	*	175
TTT	GAG	GCC	TAC	ATC	GGC	AAA	GTG	AAG	AAA	GCC	ACG	AAG	GCT	GAG	TAG	527
TGTCAGGGCTGAGGAGGAAGTCATAGCTCAGGGTCATCAGGAAAAATAATCGACAAAAAATGGCACAAAGGAATCC	606															
CATATGGTGCAGCTAAACAAACAAACATCCGTATGAGCAGGCACGAGGCCCAAGGCAGCTTGGGACTGAAGATTAG	685															
GTTGTAAGTTTATGATCCCTTCTGGTGAGGACTCGCTGAGTGCAACTCTTATCTCAAAGCACGGCTGCTGAGGGGACC	764															
CCTTCCCTCTGGCCTGTCAACTCTAGAACACACATAGATGCAAAAGGCAGCCACGGGCAAGAGATTGGGCAGAGATTAGT	843															
GGACGGCCAGCAAAACACTGCAGGAAGCAGGTGGGGGAGGAATCTACTAGCCCTTTTGTGTTTGTGTTTGTGTTT	922															
GTTTCTCTAAGGATAAAGGAGTTTCCCTTTTCAAAACGATGTGAGCACACACACACACACACACACACACACA	1001															
CACACACACACGCAATCTTTTCAACACGAAACCGAGCTAAAAGAAAAGATAAACATGGGAGAGACAGGGTTTCTAT	1080															
CTGGGACAGCAATGCTTTTGCAAAAGGCTAGGCCTTTAAAGAAAAGGTGAGCTTGTAACTCCTTGATATAAAGATGTCTT	1159															
AATTATTTTACTGCAACTGAAAGTAAAGAGGTAGAGCCTTTCCCTTCTGCACAGCCTCAGGGCTTGATGTCTCTA	1238															
CAACCAACACAGGACAGTACTTCCCCCATGATACTTTATTCTGGGAGAAAGAAACCCCTGTAGTTGAAACACCCACAC	1317															
TGACAACTGTATTCTGCTCTCCGACGAGAAATTCAGCATCCGTTGTTCAGTTGCCCAAACTTTAGGACGGAGGAGT	1396															
AAATGCAGAACTGAAAGGGAAGAGCTCAGCTGGCTGGCTTGAAAATGGAGTCTTGTAACCATGTGTAACAAATGCCAGC	1475															
CCATCGTCCCTGGAGCTGAACAGGGAGGAGGCTATGGGCAGAGACTAGAGCCGGATTCAATCCAAATGTGCAGACAGCG	1554															
TGTTCGCCTCCCTCCCTGTTTCGACCTCACACATAATCCTGGCTTCTAAATGAGGCCCTGTGACACACTCTGTGCTTTC	1633															
TATATTTTGTGACTTTCAACACAGATCTGCAGGGCTCTGCCCTGATTTGGGGTAAACACTGTGTTTCTGCAGCCCTCG	1712															
CATTGCTCCCTTCAGCAGTGCAGAGGCTTGAGAAAGTGCCCTCTGCTGGCTTAGTGAGAAGCTTCAACAAACACTTCAC	1791															
AGTAGGTTGAAAATAACTGACCACTAAGGGCTCGCGGAGATTAAACCCTAAGTTCTAAGTGTCTCAAAACACCTGACATA	1870															
TATTTGACCAAAATCAGAAGAGAGAGAAACCTCTATGCTTCAAGTAAGCGTCAATAAATTTTAAAGTGACTTTCACCTG	1949															
AGAACTCAGAAAGTCAATGTATTAAAGAGCCATATTCTGAAAGAAAAGAGAAAGAGAAAGAAAAA	2028															
AAAA	2032															

Fig. 18F

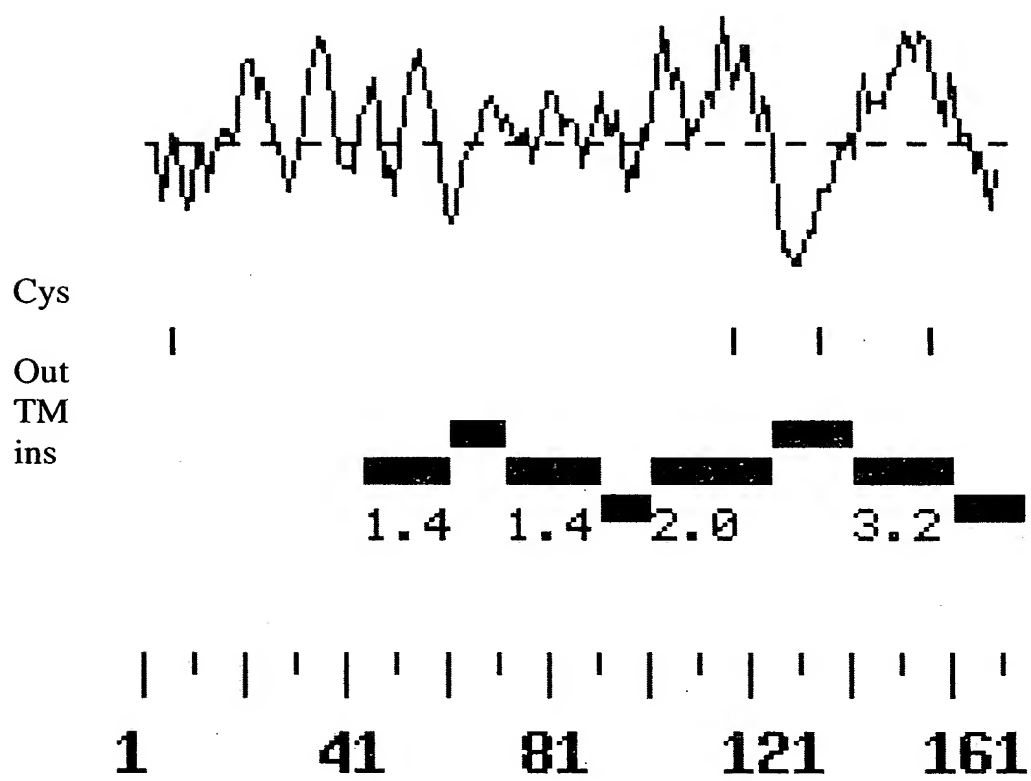


Fig. 18G

	10	20	30	40	50	60	70
human	MNMSVLT	LEFEFEKQFNENEAIQWMQENWKSF	LSALYA	AFIFGGRHLMNKR	AKFELRKPLV	LSLTL	
murine	-----						
	80	90	100	110	120	130	140
human	AVFSIFGALRTGAYMVYILMTKGLKQSVCDQGFYNGPVS	KFWAYAFVLSK	APELGDTIF	ILRKQKLIFL			
murine	-----						
		10	20	30	40		
		-----LKQSVCDQSFYNGPVS					
human	HWYHHITVLLYSWYSYKDMVAGGGWFMTMNYGVH	AVMYSYYALRAAGFRVSRK	FAMFITLSQITQMLMGC				
murine	-----						
	50	60	70	80	90	100	110
human	VVNYLVFCWMQHD--QCHSHFQNI	FWSSLMYLSYLVL	FCHFFFEAYIGKMRKTTKAE				
murine	-----						
	120	130	140	150	160	170	

Fig. 18H

human	ATGAACATGTCAGTGTGACTTTACAAAGAAATATGAATTCGAAAAGCAGTTCAACGAGAATGAAGCCATCC	10	20	30	40	50	60	70
murine	-----							
human	AATGGATGCAGGAAACTGGGAAGAAATCTTCCCTGTTTCTGCTCTGTATGCTGCTTATATATTCGGTGG	80	90	100	110	120	130	140
murine	-----							
human	TCGGCACCTAATGAATAAACGAGCAAAGTTTGAACCTGAGGAAGCCATTAGTGCTCTGGTCTCTGACCCCTT	150	160	170	180	190	200	210
murine	-----							
human	GCAGTCTTCAGTATATTCGGTGCTCTTCGAACTGGTGCTTATATGGTGACATTTTGATGACCAAAGGCC	220	230	240	250	260	270	280
murine	-----							

Fig. 18I

human	290	300	310	320	330	340	350
	TGAAGCAGTCAGTTTGTGACCAAGGGTTT	TACAAATGGACCTGT	CAGCAAAAT	TCTGGGCTTATGCATT	TGT		
murine	10	20	30	40	50	60	70
	TGAAGCAGTCAGTTTGTGACCAAGAGTTT	TACAAATGGACCTGT	CAGCAAAAT	TCTGGGCTTATGCATT	TGT		
human	360	370	380	390	400	410	420
	GCTAAGCAAGCACCCGAAC	TAGGAGATACAATAT	TTCATTAT	TCTGAGGAAGCAGAA	GCTGATCT	TCCTG	
murine	80	90	100	110	120	130	140
	GCTCAGCAAGCACCCGAAC	TAGGTGACACGATAT	TTCATCAT	TCTGAGGAAACAGAA	ACTGATCT	TCCTG	
human	430	440	450	460	470	480	490
	CAC	TGGTATCACCACATCACTGTGCTCCTGTACTCT	TGGTACTCCTACA	AAAGACATGGTTGCCGGGGGAG			
murine	150	160	170	180	190	200	210
	CAC	TGGTACCACACATCACTGTGCTCCTGTACTCCTCA	AAAGACATGGTCGCTGGGGGTG				
human	500	510	520	530	540	550	560
	GTTGGTTCA	TGACTATGAAC	TATGGCGTGCACGCCG	TGATGACTCTTACTATGCCTT	TGCCGGGCGCAGG		
murine	220	230	240	250	260	270	280
	GTTGGTTCA	TGACTATGAAC	TATGGCGTGCATGCCG	TGATGACTCTTACTACGCCTT	TGCCGGGCTGCGGG		

Fig. 18J

	570	580	590	600	610	620	630
human	TTTCCGAGTCTCCCGAAGTTTGCCATGTTTCATCACCTTGTC	CCAGATCACTCAGATGCTGATGGGCTGT					
	290	300	310	320	330	340	350
murine	TTTCCGAGTCTCCCGAAGTTTGCCATGTTTCATCACCTTGTC	CCAGATCACTCAGATGCTGATGGGCTGT					
	640	650	660	670	680	690	
human	GTGGTTAACTACCTGGTCTTCTGCTGGATGCAGCATGAC----	CAGTGTCACTCTCAC	TTTCAGAAACA				
	360	370	380	390	400	410	420
murine	GTCATTAACTACCTGGTCTTCAACTGGATGCAGCATGACAA	CGACCGTACTCCCAC	TTTCAGAAACA				
	700	710	720	730	740	750	760
human	TCTTCTGGTCCCTCACTCATGTACCTCAGCTACCTTG	TGCTCTTCTGCCATTTCTT	TGAGGCCTACAT				
	430	440	450	460	470	480	490
murine	TCTTCTGGTCCCTCGCTCATGTACCTCAGCTACCTTG	TGCTCTTCTGCCATTTCTT	TGAGGCCTACAT				
	770	780	790				
human	CGGCAAAATGAGGAAAACAACGAAAGCTGAA						
	500	510	520				
murine	CGGCAAAAGTGAAGAAAGCCACGAAAGCTGAG						

Fig. 18K


```

10      20      30      40      50      60
I400 ATGAACATGTCAGTGTGACTTTACAAGAAATATGAATT--CGAAAAAGCAGTTTCAACGAGAAATGAAGC--
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CIG30 ATGGACACATCCCATGAATTTCTCACGCGGGTTAAAAAATGGACCTTGATGCAACCCCTATGACTTCGAGACGT
      10      20      30      40      50      60      70

      70      80      90      100     110     120
I400 --CA--TCCAATGG-----ATGCAGGAAAACTGGAAGAAATCTTTCCCT-GTTTCTTCTGC-TCTGTATGCT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CIG30 TTCAGGACTTAAGGCCCTTTTGGAGGAGTACTGGGTAAGCTCATTTCTCATAGTGGTCGTCCTATCTGTT
      80      90      100     110     120     130     140

      130     140     150     160     170     180     190
I400 GCCTTTATATTTCGGTGGTCGGCACCTA-ATGAATAAACGAGCAAAAGTTTGAAC-T-GAGGAAGCCATTAGT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CIG30 GC--TCATCGTTGTTGGCCAG-ACCTACATGAGAACGCCGA-AGAGCTTCAGCTTGCAGAGGCCCTCTCAT
      150     160     170     180     190     200

      200     210     220     230     240     250     260
I400 GCTCTGGTCTCTGACCCCTTGACGTCTTCAGTATATTCGGTGCTCTTCGAACTGGTGCTTATATGGTGAC
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CIG30 CCTCTGGTCCCTTCTTCCTGGCAATATTCAGTATCCCTGGGTACTCTGAGGATGTGGAAGTTTATGGCAACA
      210     220     230     240     250     260     270

```

Fig. 18M

I400 ATTTTGATGACCAAGCCCTGAAGCAGTCAGTTTG--TGACCAGGGTTTTTACAATGGAC-CTGT CAGCA
::
CIG30 GTGATGTTTACAGTGGGCCCTCAAGCAAACCGTGTGCTTTGCCA---TCTACACGGATGACGCCGTAGTCA
280 290 300 310 320 330 340

330 AATTCTGGGCTTATGCATTTGTGCTAAGCAAAGCACCCGAAC TAGGAGATACAATATTCATTATTCTGAG
I400
::::
CIG30 GATTC TGGTCCCTTCTCTCTTCTCTCAGCAAAGGTTGTTGAAC TGGGAGACACGGCCTTCATCATCCTGCG
350 360 370 380 390 400 410

400 GAAGCAGAAGCTGATCTTCTCTGCACTGGTATCACCACATCACTGTGCTCCTGTACTCTTGGTACTCCTAC
I400
::::
CIG30 TAAGCGTCCACTCATCTTTGTGCCACTGGTACCACCAAGCAGCAGTGTGCTACTGTTCAACAAGCTTTGGATAC
420 430 440 450 460 470 480

470 AAAGACATGGTTGCCGG-GGGAGGTTGGTT CATGACTATGAAC TATGGCGTGCACGCCGTGATGTACTCT
I400
::::
CIG30 AAGAACA AAGT-GCC TT CGGGTGGCTGGTT CATGACCATGAAC TTTGGCGTCCATTCTGT CATGTACACT
490 500 510 520 530 540 550

Fig. 18N

```

540      550      560      570      580      590      600
I400 TACTATGCCCTTGC GCGGCAGGTTTCCGAGTCTCCCGAAGTTTGCC--ATGTTTCATCACCTTGTCC--
      ::::: . . . . . ::::: . . . . . ::::: . . . . . ::::: . . . . . ::::: . . . . .
CIG30 TACTACACTATGAAGGCTGCCAAA--CTGAAGCATCCCTAATCTTCTCCCCCATGGTTCATCACCCAG--CCTG
      560      570      580      590      600      610

610      620      630      640      650      660      670
I400 CAGATCACT-CAGATGCTGATGGGCTGTGTGGTTAACTACCTGGTCTTCTGCTGGATGCAGCATGACCAG
      ::::: . . . . . ::::: . . . . . ::::: . . . . . ::::: . . . . . ::::: . . . . .
CIG30 CAGAT-TCTGCAGATGGTTCCTGGGCACCATCTTTGGCATACTGAATTACATCTGGAGGCAGGAGAAAAGGA
      620      630      640      650      660      670      680

680      690      700      710      720      730      740
I400 TGTCACTCTCACTTTTCAGAAACA--TCTTCTGGTCCCTCACTCATGTACCTCAGCTACCTTGTGCTCTTCTG
      ::::: . . . . . ::::: . . . . . ::::: . . . . . ::::: . . . . . ::::: . . . . .
CIG30 TGCCACACA-ACAA-CGGAACACTTCTTCTGGTCTTTTATGCTATATGGACCTATTTTCATCCTATTTCGC
      690      700      710      720      730      740      750

750      760      770      780      790
I400 CCATTTCTTCTTTGAGGCCCTACATCGG--CAAAAATGAGGAAAAACAAC-GAAAGCTGAA
      ::::: . . . . . ::::: . . . . . ::::: . . . . . ::::: . . . . . ::::: . . . . .
CIG30 TCAC TTCTCCACCGAGCCTACCTCAGGCCCAAGGGCAAAGTTGCATCCAAGAGCC-AA
      760      770      780      790      800      810

```

Fig. 180

L	G	D	T	I	F	I	I	L	R	K	Q	K	L	I	F	L	H	W	Y	20
CTA	GGT	GAT	ACG	ATA	TTC	ATC	ATT	CTG	AGG	AAG	CAG	AAG	CTG	ATC	TTC	CTG	CAC	TGG	TAC	60
H	H	I	T	V	L	L	Y	S	W	Y	S	Y	K	D	M	V	A	G	G	40
CAC	CAC	ATC	ACT	GTG	CTC	CTG	TAC	TCT	TGG	TAC	TCC	TAC	AAA	GAC	ATG	GTA	GCT	GGG	GGT	120
G	W	F	M	T	M	N	Y	G	V	H	A	V	M	Y	S	Y	Y	A	L	60
GGT	TGG	TTC	ATG	ACT	ATG	AAC	TAT	GGC	GTA	CAC	GCC	GTC	ATG	TAC	TCT	TAC	TAC	GCC	TTG	180
R	A	A	G	F	R	V	S	R	K	F	A	M	F	I	T	L	S	Q	I	80
CGG	GCT	GCG	GGT	TTC	CGG	GTC	TCC	CGG	AAG	TTT	GCC	ATG	TTC	ATC	ACG	TTG	TCC	CAG	ATC	240
T	Q	M	L	M	G	C	V	I	N	Y	L	V	F	N	W	M	Q	H	D	100
ACT	CAG	ATG	CTG	ATG	GGC	TGT	GTC	ATT	AAC	TAC	CTG	GTC	TTC	AAC	TGG	ATG	CAG	CAT	GAC	300
N	D	Q	C	Y	S	H	F	Q	N	I	F	W	S	S	L	M	Y	L	S	120
AAT	GAC	CAG	TGC	TAC	TCC	CAC	TTT	CAG	AAC	ATC	TTC	TGG	TCC	TCA	CTC	ATG	TAC	CTC	AGC	360
Y	L	L	L	F	C	H	F	F	F	E	A	Y	I	G	K	V	K	K	A	140
TAC	CTT	CTG	CTC	TTC	TGC	CAT	TTC	TTC	TTT	GAG	GCC	TAC	ATC	GGC	AAA	GTG	AAG	AAA	GCG	420
T	K	A	E	*																145
ACG	AAG	GCC	GAG	TAG																435

Fig. 18P

TGTCAGAGCTGAGGAGGAAAGACATAGCTCAGGGTCATCACGAAAAAATAATAGACAAAAAAGAAAAATGGCACAAAGGAATCA 514
CATATGGTGCAGCTAAACAAAAACAACATTATGAGCAGACGCTAAGCCCCAAGCAGCTTGGGAGTGAAGATTAGGTT 593
GTAAGTTTATGATCCCTTTTGGGTGAGGACTCACTGAGAACACTGCTGCTGAGGACCCCTTCCCTCTTACCTGTCAA 672
CTCTAGAACACACTAGAAGCCAAAGCAGCCATGGGCAAGGAGATTAGTGGACAGCAAGCAAAACACTGCAGGAAGAGGG 751
GGGAGATCTATTTCAGAGTTTGTGTTTGTGTTTGTGTTTGTGTTTCTCTAAGGATAAAGGAGTTTCCCCCTTTTCAAACTG 830
TGTGAGCACACCCACGCGCATGCAGACACACCCACCTACACACTATCTGCAGATGACCAAGTGTCTATGCTGTTTTTTAC 909
AAATAAACTTGAGACAAGAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 974

Fig. 18Q

	10	20	30	40	50	60	70
human	MNMSVLT	LQEYEF	EKQFN	ENEA	IQWMQ	ENWKS	FLFS
murine	-----	-----	-----	-----	-----	-----	-----
rat	-----	-----	-----	-----	-----	-----	-----
human	AVFSIF	GALRT	GAYMV	YILMT	KGLKQ	SVCDQ	GFYNG
murine	-----	-----	-----	-----	-----	-----	-----
rat	-----	-----	-----	-----	-----	-----	-----
human	HWYHHI	TVLLY	SWYSY	KDMV	AGGGW	FMTMN	YGVH
murine	-----	-----	-----	-----	-----	-----	-----
rat	-----	-----	-----	-----	-----	-----	-----
human	VVNYLV	FCWMQ	HD--Q	CHSHF	QNI	FWSSL	MYLS
murine	-----	-----	-----	-----	-----	-----	-----
rat	-----	-----	-----	-----	-----	-----	-----

Fig. 18R

GTCGACCCACGGTCCGGGGAGCGGGCTAAGAGTGCCCGCACCGCCTCACAACTGGGAACCGGAGAGTAGGGGCCGTC	79
GGCTGGCAAAGAACCCGCGTGCCCTCCTCGGCAAGGGCCATCCGGTGCCACCCCATGTGCGCACTAGAGCAGAAGAGGGTGA	158
<div style="text-align: center;"> M T W L V </div>	
GTCCCTGAAC TGC AACCTGC ACAGAGCTGCTCTGTACTGTCCCTGGTGGTGGCCGCC ATG ACC TGG TTG GTG	5 229
L L G T L L C M L R V G L G T P D S E G	25
CTG CTG GGG ACA CTG CTC TGC ATG CTG CGC GTC GGT GGG TTA GGC ACC CCG GAC TCC GAG GGT	289
F P P R A L H N C P Y K C I C A A D L L	45
TTC CCG CCC CGT GCG CTC CAC AAC TGC CCC TAC AAA TGT ATC TGC GCT GCC GAC CTG CTA	349
S C T G L G L Q D V P A E L P A A T A D	65
AGC TGC ACT GGC CTA GGG CTG CAG GAC GTG CCA GCC GAG TTA CCT GCC GCT ACT GCG GAC	409
L D L S H N A L Q R R P G W L A P L F	85
CTC GAC CTG AGC CAC AAC GCG CTC CAG CGC CTG CGC CCC GGC TGG TTG GCG CCC CTC TTC	469
Q L R A L H L D H N E L D A L G R G V F	105
CAG CTG CGC GCC CTG CAC CTA GAC CAC AAC GAA CTA GAT GCG CTG GGT CGC GGC GTC TTC	529
V N A S G L R L L D L S S N T L R A L G	125
GTC AAC GCC AGC GGC CTG AGG CTG GAT CTA TCA TCT AAC ACG TTG CGG GCG CTT GGC	589

Fig. 19A

R	H	D	L	D	G	L	G	A	L	E	K	L	L	L	L	F	N	N	R	L	145
CGC	CAC	GAC	CTC	GAC	GGG	CTG	GGG	GCG	CTG	GAG	AAG	CTG	CTT	CTG	TTT	AAT	AAC	CGC	TTG	649	
V	H	L	D	E	H	A	F	H	G	L	R	A	L	S	H	L	Y	L	G	165	
GTG	CAC	TTG	GAC	GAG	CAT	GCC	TTC	CAC	GGC	CTG	CGC	GCG	CTC	AGC	CAT	CTC	TAC	CTG	GGC	709	
C	N	E	L	A	S	F	S	F	D	H	L	H	G	L	S	A	T	H	L	185	
TGC	AAC	GAA	CTC	GCC	TCG	TTC	TCC	TTC	GAC	CAC	CTG	CAC	GGT	CTG	AGC	GCC	ACC	CAC	CTG	769	
L	T	L	D	L	S	S	N	R	L	G	H	I	S	V	P	E	L	A	A	205	
CTT	ACT	CTG	GAC	CTC	TCC	TCC	AAC	GCG	CTG	GGA	CAC	ATC	TCC	GTA	CCT	GAG	CTG	GCC	GCG	829	
L	P	A	F	L	K	N	G	L	Y	L	H	N	N	P	L	P	C	D	C	225	
CTG	CCG	GCC	TTC	CTC	AAG	AAC	GGC	CTC	TAC	TTG	CAC	AAC	AAC	CCT	TTG	CCT	TGC	GAC	TGC	889	
R	L	Y	H	L	L	Q	R	W	H	Q	R	G	L	S	A	V	R	D	F	245	
CGC	CTC	TAC	CAC	CTG	CTA	CAG	CAG	TGG	CAC	CAG	CGG	GGC	CTG	AGC	GCC	GTG	CGC	GAC	TTT	949	
A	R	E	Y	V	C	L	A	F	K	V	P	A	S	R	V	R	F	F	Q	265	
GCG	CGC	GAG	TAC	GTA	TGC	TTG	GCC	TTC	AAG	GTA	CCC	GCG	TCC	CGC	GTG	CGC	TTC	TTC	CAG	1009	
H	S	R	V	F	E	N	C	S	S	A	P	A	L	G	L	K	R	P	E	285	
CAC	AGC	CGC	GTC	TTT	GAG	AAC	TGC	TCG	TCG	GCC	CCA	GCT	CTT	GGC	CTA	AAG	CGG	CCG	GAA	1069	

Fig. 19B

E	H	L	Y	A	L	V	G	R	S	L	R	L	Y	C	N	T	S	V	P	305
GAG	CAC	CTG	TAC	GCG	CTG	GTG	GGT	CGG	TCC	CTG	AGG	CTT	TAC	TGC	AAC	ACC	AGC	GTC	CCG	1129
A	M	R	I	A	W	V	S	P	Q	Q	E	L	L	R	A	P	G	S	R	325
GCC	ATG	CGC	ATT	GCC	TGG	GTT	TCG	CCG	CAG	CAG	GAG	CTT	CTC	AGG	GCG	CCA	GGA	TCC	CGC	1189
D	G	S	I	A	V	L	A	D	G	S	L	A	I	G	N	V	Q	E	Q	345
GAT	GGC	AGC	ATC	GCG	GTG	CTG	GCC	GAC	GGC	AGC	TTG	GCC	ATA	GGC	AAC	GTA	CAG	GAG	CAG	1249
H	A	G	L	F	V	C	L	A	T	G	P	R	L	H	H	N	Q	T	H	365
CAT	GCG	GGA	CTC	TTC	GTG	TGC	CTG	GCC	ACT	GGG	CCC	CGC	CTG	CAC	CAC	AAC	CAG	ACG	CAC	1309
E	Y	N	V	S	V	H	F	P	R	P	E	P	E	A	F	N	T	G	F	385
GAG	TAC	AAC	GTG	AGC	GTG	CAC	TTT	CCG	CGC	CCA	GAG	CCC	GAG	GCT	TTC	AAC	ACA	GGC	TTC	1369
T	T	L	L	G	C	A	V	G	L	V	L	V	L	L	Y	L	F	A	P	405
ACC	ACA	CTG	CTG	GGC	TGT	GCC	GTG	GGC	CTT	GTG	CTC	GTG	CTG	CTC	TAC	CTG	TTC	GCC	CCA	1429
P	C	R	C	C	R	R	A	C	P	L	P	P	L	A	P	N	T	Q	P	425
CCC	TGC	CGC	TGC	TGC	CGT	GCC	TGC	TGC	CCG	CTG	CCG	CCG	CTG	GCC	CCA	AAC	ACC	CAG	CCC	1489
A	P	R	A	E	P	H	K	S	S	V	L	S	T	T	P	P	D	A	P	445
GCT	CCA	AGA	GCT	GAG	CCG	CAC	AAG	TCC	TCA	GTA	CTC	AGC	ACC	ACA	CCG	CCA	GAC	GCA	CCC	1549

Fig. 19C

S	P	Q	G	Q	A	S	T	S	T	*	
AGC	CCG	CAA	GGC	CAA	GCG	TCC	ACA	AGC	ACG	TAG	456
											1582
TCT	TTCT	GGAGCC	AGGCCG	GAGGGCC	CTCA	ATGGCC	CCGCGT	GCAGCT	GGCAGT	AGCTGAGGAATTCGATCTCTACAACC	1661
CTG	AGGCC	CTGC	AGCTGA	AGCGTGG	CTCTG	AGTCCGCC	CCAGCTCCA	TAGGCTCCG	AGGGTCCCATGACAACCTAGACTGC	1740	
CAG	GGCTCCCC	ACCCAG	CCCCCAC	CCCTCT	TGCTG	CTGCCC	CTGCTCCC	TGCTCCAG	AACTGGCAGATACT	1819	
GGT	GGGA	GCAC	TGTGCC	CTTGCCCC	CAGCTT	CCTGTAT	GGCCCTCG	AAACAAAT	GGCCCTTCTCGCTCACTGGTAGA	1898	
GAC	AGGGT	TGTG	TCCCCA	ACCTG	CCCTTCTG	CTCTG	CCCCTG	CACAG	ACC	AAAGGCCCTGCAAGGTG	1977
CTA	GTCC	TGCT	TTCCCG	CGGACTT	CC	TAGTG	CCCCAA	ATGCCCT	GTGAGGCTGAGAGACCCAGGCCCTGTGGCTTTCA	2056	
AC	CAGC	ACAG	CTGTG	GAAGTGG	CTGT	TCTAC	AGCC	TGTGA	AGAACCCCTGTAGCAGAGCCTCCCATCCACCC	2135	
TC	AGGG	GTGAG	GCAG	CTCTCG	AGGAGTGG	TGCTCA	AGAGCTG	ACG	CGGCCACCTCCCC	TAAGGGGTGGAG	2214
GG	AGTGG	CCCC	CACAG	GGA	AAAGAG	GGGCTCT	GAAGGA	AGATCTCG	CCCCCACACCC	CCAGGACAGAAAGGAAACAAGC	2293
CCG	CCCTCT	GGTG	AAATGG	GACTCCC	CTCC	ATCC	ACCA	CAACCC	TAACCTCCTG	AAAAGCTTCACAACTTCACGCAGAGTCC	2372
GGT	GCAG	GCAC	CCAG	GA	AAAGG	CTCCT	CAAG	AGGTTCC	TGGTGTCTG	GCCTAAGCCCCAGCCAGAGGCCCTGCTC	2451

Fig. 19D

TCTCTGGCCCTGGGGCATCCACCGTTGTTCTGAAGGCAGAGCCCAATTCTGTGGGCTCACAAAGACACAGTGAAGGGGATC 2530
ATGGCCCTGCACCCCTGCTTTTCAGCAGTAAAAAGCCCCGAAAAGCCCTGGCGAGCATGGCCGAGCTGGGAGGGCCCGAGCCG 2609
GAACTCCACGTCCTCGAGAGCAGGAGCCTCTTAAAGGGCTGGCACTGGTCTCAGCCCTAATGGCTGAGGCGGTACCCCTGG 2688
CTTCATATGCATCTCACTGCTCCCACCTGCAGGGGGGCAGGGAAGGGGGGTCTGGGAGCCCTTCATGTGTGGGGGCCGAG 2767
CTGGGGGCCCCCATGGCCATCCTGGACCTCGCTGCTCCAGAGTTTAATAAAGGTAGCACATGCTTATTGCTAGAAAAAA 2846
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGC 2895

Fig. 19E

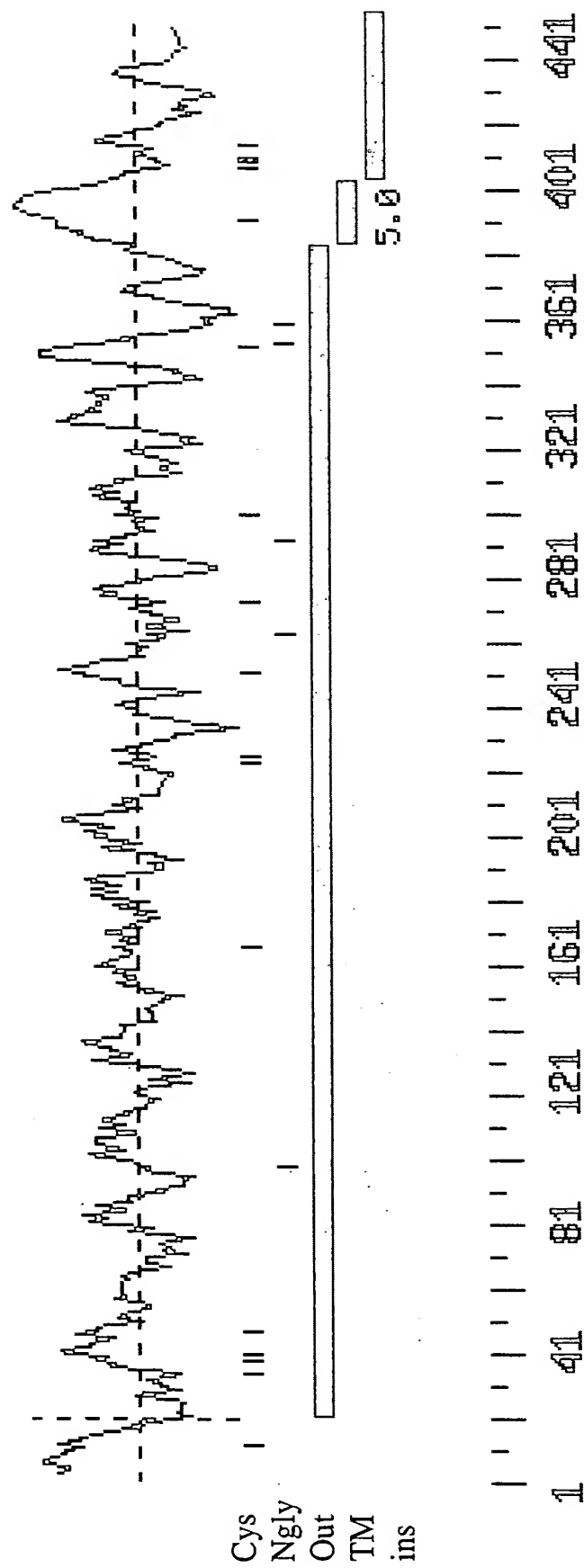


Fig. 19F

10	20	30	40	50	60	70
H	MTWLVLLG	TLLCMLRV	GLGTPDSE	GFPPRALH	NCYPKIC	AADLLSCTG
						LGLQDVPA
						ELPAATADL
						DLSH
	:	:	:	:	:	:
	:	:	:	:	:	:
	:	:	:	:	:	:
P	MN-LDIH	CEQLSDAR	WTELLP	LQQYEVVR	LDCCGLTE	EHCKDIGS--
						ALRANPSLT
						ELCLRTNEL--
						GD
10	20	30	40	50	60	
80	90	100	110	120	130	
H	NALQRLR	PGWLAPL	FQLRALH	LHDNELD	ALGRGVFNA--	--SGLRL
						LDLSSNTLR
						ALGRHDL-D
						GLGA-
	:	:	:	:	:	:
	:	:	:	:	:	:
	:	:	:	:	:	:
P	AGVHLV	LQGLQSP	TKIQKLS	LQNC	SLTEAGC	GVLPSTLR
						SLPTLREL
						HLSDNPL
						GDAGLRLL
						CEGLDLP
70	80	90	100	110	120	130
140	150	160	170	180	190	200
H	---LEK	LLLFNNR	LVLHLD-E	HAFHGLR	ALSHLYG	CNELASF
						DFDHLHGL
						SATHLLT
						LDLSSNR
						LGHISV
	:	:	:	:	:	:
	:	:	:	:	:	:
	:	:	:	:	:	:
P	QCHLEK	LQLEYCR	LTAASCE	PLASVLR	ATRAL----	KELTVSNND--
						IGEAGARV
						LQGQLAD--
						-----SA
140	150	160	170	180	190	
210	220	230	240	250	260	
H	PELAAL	PAPFLKN-	GLYLHNN	PLPCDCR	LYHLLQR	WHQGLSA
						VRDFAREY
						VVCLAFK
						VPASRVR--
						---FFQH
	:	:	:	:	:	:
	:	:	:	:	:	:
	:	:	:	:	:	:
P	CQLETL	R--LENC	GLTPAN	CKDL	CGIVASQ	ASLRELDL
						GSNGLGD
						AGIAELCP
						GLLSPAS
						RKTLWL
						WEC
200	210	220	230	240	250	260

Fig. 19G

270	280	290	300	310	320
H	SRVFENCSSA-PALGLKRPEEHLYALVGRSL-----RLYCNTSV-PAMRIAWVSPQQELLRAPGSRDGS				
	: : : : :	: : : : :	: : : : :	: : : : :
P	DITASGCRDLCRVLQAKETLKEL-SLAGNKLGDGARGLLCESLLQPGCQLES LWKSCSLTAACCCQHVS				
	270 280 290 300 310 320 330				
330	340	350	360	370	380 390
H	AVLADGSLAIGNVQEQHAGLFVCLATGPRLLHNNQTHEYNVSVHFPRPEPEAFNTGFTLLGCAVGLVL				
	: : : : :	: : : : :	: : : : :	: : : : :
P	MLTQNKHL-----LELQLSSNKLGDSGIQELCQALSQPGTTLRVLC LGDCEVTNSGCSSLAS--LLLANRS				
	340 350 360 370 380 390				
400	410	420	430	440	450
H	LYLFAPPCRCRRACPLPPLAPNTQPAPRAEPHK-SSVLSTTPPDAPSPQGQASTS-----T				
	: : : : :	: : : : :	: : : : :	: : : : :	: : : : :
P	LRELDLSNNCVGDPGVLLQLLSLEQPGGCALEQLVLDYDTYWTEEEVEDRLQALEGSKPGLRVIS				
	400 410 420 430 440 450				

Fig. 19H

ccg ttt ctc ttt aac cac ttg cac ggt ctg ggg tta acc cgc ctg cgg	48
Pro Phe Leu Phe Asn His Leu His Leu Gly Leu Thr Arg Leu Arg	
1 5 10 15	
act ctg gac ctc tcc tcc aac tgg ctg aaa cat atc tcc atc cct gag	96
Thr Leu Asp Leu Ser Ser Asn Trp Leu Lys His Ile Ser Ile Pro Glu	
20 25 30	
ttg gct gca ctg cca act tat ctc aag aac agg ctc tac ctg cac aac	144
Leu Ala Ala Leu Pro Thr Tyr Leu Leu Arg Leu Tyr Leu His Asn	
35 40 45	
aac ccg ctg ccc tgt gac tgc agc ctc tac cac ctg ctc cgg cgc tgg	192
Asn Pro Leu Pro Cys Asp Cys Ser Leu Tyr His Leu Leu Arg Arg Trp	
50 55 60	
cac cag cgg ggc ctg agt gcc ctg cat gat ttt gaa cgc gag tac aca	240
His Gln Arg Gly Leu Ser Ala Leu His Asp Phe Glu Arg Glu Tyr Thr	
65 70 75 80	
tgc ttg gtc ttt aag gtg tca gag tcc cga gtg cgc ttt ttt gag cac	288
Cys Leu Val Phe Lys Val Ser Glu Ser Arg Val Arg Phe Phe Glu His	
85 90 95	
agc cgg gtc ttc aag aac tgc tct gtg gct gca gct cca ggc tta gag	336
Ser Arg Val Phe Lys Asn Cys Ser Val Ala Ala Ala Pro Gly Leu Glu	
100 105 110	

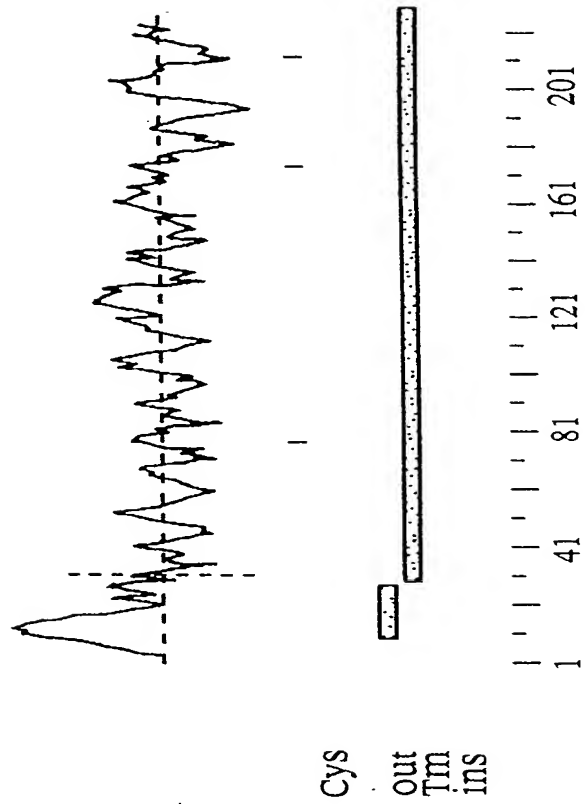
Fig. 19I

ctg cct gaa gag gag cag ctg cac gcg cag gtg ggc cag tcc ctg agg ctc	384
Leu Pro 115 Glu Glu Gln Gln Leu His 120 Ala Gln Val Gly Gln Ser 125 Leu Arg Leu	
ttc tgc aac acc agt gtg cct gcc act cgg gtg gcc tgg gtc tcc ccg	432
Phe Cys Asn Thr Ser Val Pro Ala Thr Arg Val Ala Trp Val Ser Pro	
130 135 140	
aag aat gag ctg ctt gtg gcg cca gcc tct cag gat ggt agc atc gct	480
Lys Asn Glu Leu Leu Val Ala Pro Ala Ser Gln Asp Gly Ser Ile Ala	
145 150 155 160	
gtg ttg gct gat ggc agc tta gcc ata ggc agg gtg caa gag cag cac	528
Val Leu Ala Asp 165 Gly Ser Leu Ala Ile Gly Arg Val Gln Glu Gln His	
170 175	
gca ggc gtc ttt gtg tgc ctg gcc agt ggg ccc cgc ctg cac cac aac	576
Ala Gly Val Phe 180 Val Cys Leu Ala Ser Gly Pro Arg Leu His His Asn	
185 190	
cag aca ctt gag tac aat gtg agt gtg caa aag gct cgc ccc gag cca	624
Gln Thr Leu Glu Tyr Asn Val Ser Val Gln Lys Ala Arg Pro Glu Pro	
195 200 205	
gag act ttc aac aca ggc ttt acc acc ctg ctg ggc tgt att gtg ggc	672
Glu Thr Phe Asn Thr Gly Phe Thr Thr Leu Leu Gly Cys Ile Val Gly	
210 215 220	

Fig. 19J

ctg gtg ctg gtg ttg ctg tac ttg ttt gca cca ccc tgt cgt ggc tgc	720
Leu Val Leu Val Leu Leu Tyr Leu Leu Phe Ala Pro Pro Cys Arg Gly Cys	
225 230 235 240	
tgt cac tgc tgt cag cgg gcc ggc tgc cgc aac cgt tgc tgg ccc cgg gca	768
Cys His Cys Cys Gln Arg Ala Cys Arg Asn Arg Cys Trp Pro Arg Ala	
245 250 255	
tcc agt cca ctc cag gag ctg agc gca cag tcc tcc atg ctt agc act	816
Ser Ser Pro Leu Gln Glu Leu Ser Ala Gln Ser Ser Met Leu Ser Thr	
260 265 270	
acg cca cca gat gca ccc agc cgc aag gcc agt gtc cac aag cat gtg	864
Thr Pro Pro Asp Ala Pro Ser Arg Lys Ala Ser Val His Lys His Val	
275 280 285	
gtc ttc ctg gag ccg ggc aag aag ggc ctc aat aat ggc cgt gtg cag ctc	912
Val Phe Leu Glu Pro Pro Gly Lys Lys Gly Leu Asn Asn Gly Arg Val Gln Leu	
290 295 300	
gca gta cct cca gac tcc gat ctg tgc aac ccc atg ggc ttg caa ctc	960
Ala Val Pro Pro Asp Ser Asp Leu Cys Asn Pro Met Gly Leu Gln Leu	
305 310 315 320	
aa	962

Fig. 19K



Cys
out
Tm
ins

Fig. 19L

```

M      1  ..... PFLFNHLHGLTRLRLTLDLSSNWLKHISI 30
H     151  HAFHGLRALSHLYLGCNELASFDFDHLHGLSATHLLTLDLSSNRLGHISV 200

M      31  PELAAALPTYLKNRLYLHNNPLPCDCSLYHLLRRWHQGLSALHDFEREYT 80
H     201  PELAAALPAFLKNGLYLHNNPLPCDCRLYHLLQRWHQGLSAVRDFAREYV 250

M      81  CLVFKVSESRVFFEHRSRVFKNCVAAAPGLELPEEQHQAQVGQSLRLFC 130
H     251  CLAFKVPASRVFFQHRSRVFENCSSAPALGLKRPEEHLYALVGRSLRLYC 300

M     131  NTSVPATRVAVWSPKNELLVAPASQDGSIAVLADGSLAIGRVQEQHAGVF 180
H     301  NTSVPAMRIA WSPQQELLRAPGSRDGSIAVLADGSLAIGNVQEQHAGLF 350

M     181  VCLASGPRLHHNQTL EYNVSVQKARPEPEFTFNTGFTTLLGCIVGLVLL 230
H     351  VCLATGPRLHHNQTHEYNVSVHFPRPEPEAFNTGFTTLLGCAVGLVLL 400

M     231  YLFAPPCRGCHCCQACRNRCWPRASSPLQELSA.QSSMLSTTPPDAPS 279
H     401  YLFAPPCR...CCRRACPLPPLAPNTQAPAPRAEPHKSSVLSTTPPDAPS 446

M     280  RKASVHKHVVFLEPGKKGLNGRVQLAVPPDSDL CNP MGLQL 320

H     447  PQGQASTST..... 455

```

Fig. 19M

GTCGACCCACGCGTCCGGGAACCCAGCGTCCGCCGAC	ATG	GCC	TGG	ACC	AAG	TAC	CAG	CTG	TTC	CTG	L	F	L	10
														69
A G L M L V T G S I N T L S A K W A D N														30
GCC GGG CTC ATG CTT GTT ACC GGC TCC ATC AAC ACG CTC TCG GCA AAA TGG GCG GAC AAT														129
F M A E G C G G S K E H S F Q H P F L Q														50
TTC ATG GCC GAG GGC TGT GGA GGG AGC AAG GAG CAC AGC TTC CAG CAT CCC TTC CTC CAG														189
A V G M F L G G E F S C L A A A F Y L L R C														70
GCA GTG GGC ATG TTC CTG GGA GAA TTC TCC TGC CTG GCT GCC TTC TAC CTC CTC CGA TGC														249
R A A G G Q S D S S V D P Q Q Q P F N P L L														90
AGA GCT GCA GGG CAA TCA GAC TCC AGC GTA GAC CCC CAG CAG CCC TTC AAC CCT CTT CTT														309
F L P P A A L C D M T G T G T S L M Y V A L N														110
TTC CTG CCC CCA GCG CTC TGT GAC ATG ACA GGG ACC AGC CTC ATG TAT GTG GCT CTG AAC														369
M T S A S S F Q M L R G A V I I F T G L														130
ATG ACC AGT GCC TCC AGC TTC CAG ATG CTG CGG GGT GCA GTG ATC ATA TTC ACT GGC CTG														429
F S V A F L G R R R L V L S Q W L G I L A														150
TTC TCG GTG GCC TTC CTG GGC CGG AGG CTG GTG CTG AGC CAG TGG CTG GGC ATC CTA GCC														489

Fig. 20A

T	I	A	G	L	V	V	V	G	L	A	D	L	L	S	K	H	D	S	Q	170
ACC	ATC	GCG	GGG	CTG	GTG	GTC	GTG	GGC	CTG	GCT	GAC	CTC	CTG	AGC	AAG	CAC	GAC	AGT	CAG	549
H	K	L	S	E	V	I	T	G	D	L	L	I	I	M	A	Q	I	I	V	190
CAC	AAG	CTC	AGC	GAA	GTG	ATC	ACA	GGG	GAC	CTG	TTG	ATC	ATC	ATG	GCC	CAG	ATC	ATC	GTT	609
A	I	Q	M	V	L	E	E	K	F	V	Y	K	H	N	V	H	P	L	R	210
GCC	ATC	CAG	ATG	GTG	CTA	GAG	GAG	AAG	TTC	GTC	TAC	AAA	CAC	AAT	GTG	CAC	CCA	CTG	CGG	669
A	V	G	T	E	G	L	F	G	F	V	I	L	S	L	L	L	V	P	M	230
GCA	GTT	GGC	ACT	GAG	GGC	CTC	TTT	GGC	TTT	GTG	ATC	CTC	TCC	CTG	CTG	CTG	GTG	CCC	ATG	729
Y	Y	I	P	A	G	S	F	S	G	N	P	R	G	T	L	E	D	A	L	250
TAC	TAC	ATC	CCC	GCC	GGC	TCC	TTC	AGC	GGA	AAC	CCT	CGT	GGG	ACA	CTG	GAG	GAT	GCA	TTG	789
D	A	F	C	Q	V	G	Q	Q	P	L	I	A	V	A	L	L	G	N	I	270
GAC	GCC	TTC	TGC	CAG	GTG	GGC	CAG	CAG	CCG	CTC	ATT	GCC	GTG	GCA	CTG	CTG	GGC	AAC	ATC	849
S	S	I	A	F	F	N	F	A	G	I	S	V	T	K	E	L	S	A	T	290
AGC	AGC	ATT	GCC	TTC	TTC	AAC	TTC	GCA	GGC	ATC	AGC	GTC	ACC	AAG	GAA	CTG	AGC	GCC	ACC	909
T	R	M	V	L	D	S	L	R	T	V	V	I	W	A	L	S	L	A	L	310
ACC	CGC	ATG	GTG	TTG	GAC	AGC	TTG	CGC	ACC	GTT	GTC	ATC	TGG	GCA	CTG	AGC	CTG	GCA	CTG	969

Fig. 20B

G	W	E	A	F	H	A	L	Q	I	L	G	F	L	I	L	L	I	G	T	330					
GGC	TGG	GAG	GCC	TTC	CAT	GCA	CTG	CAG	ATC	CTT	GGC	TTC	CTC	ATA	CTC	CTT	ATA	GGC	ACT	1029					
A	L	Y	N	G	L	H	R	P	L	L	G	R	L	S	R	G	R	P	L	350					
GCC	CTC	TAC	AAT	GGG	CTA	CAC	CGT	CCG	CTG	CTG	GGC	CGC	CTG	TCC	AGG	GGC	CGG	CCC	CTG	1089					
A	E	E	S	E	Q	E	R	L	L	G	G	T	R	T	P	I	N	D	A	370					
GCA	GAG	GAG	AGC	GAG	CAG	GAG	AGA	CTG	CTG	GGT	GGC	ACC	CGC	ACT	CCC	ATC	AAT	GAT	GCC	1149					
S	*																			372					
AGC	TGA																			1155					
GGT	TCC	CTG	GAG	GGC	TCT	ACT	GCC	ACCC	GGG	TGCT	CCT	TCT	CCT	TGAG	ACT	GAG	GCC	CAC	ACAG	GGCT	GGT	GGG	CCCC	GAA	1234
TGCC	CTAT	CCCC	AA	GGC	CTC	ACCC	TG	TCCCC	CTGC	AGAA	CCCC	CAG	GGC	AGCT	GTG	CTGCC	CAC	AGAA	GATA	AA	CAAC	AC			1313
CCA	AGT	CCCT	CTTT	TCT	CACT	ACC	CTGC	AGGG	TGGT	GTATT	ACCC	AG	CCCC	CACA	AGC	CTG	AGT	GCG	CAG	ACCT	C				1392
AGC	TCT	GGAC	CCCT	CCT	AC	AGC	ACT	AGAG	CTAA	ATCAT	GAA	GTGA	ATTG	TAG	GAA	TTT	TACC	ACCC	GTA	GTAT	CTG				1471
AAT	CATA	AACT	AGAT	TAT	CATA	AAAA	AAAA	AAAA	AAAA	AAAA	AA	AGG	CGG	CCGC											1518

Fig. 20C

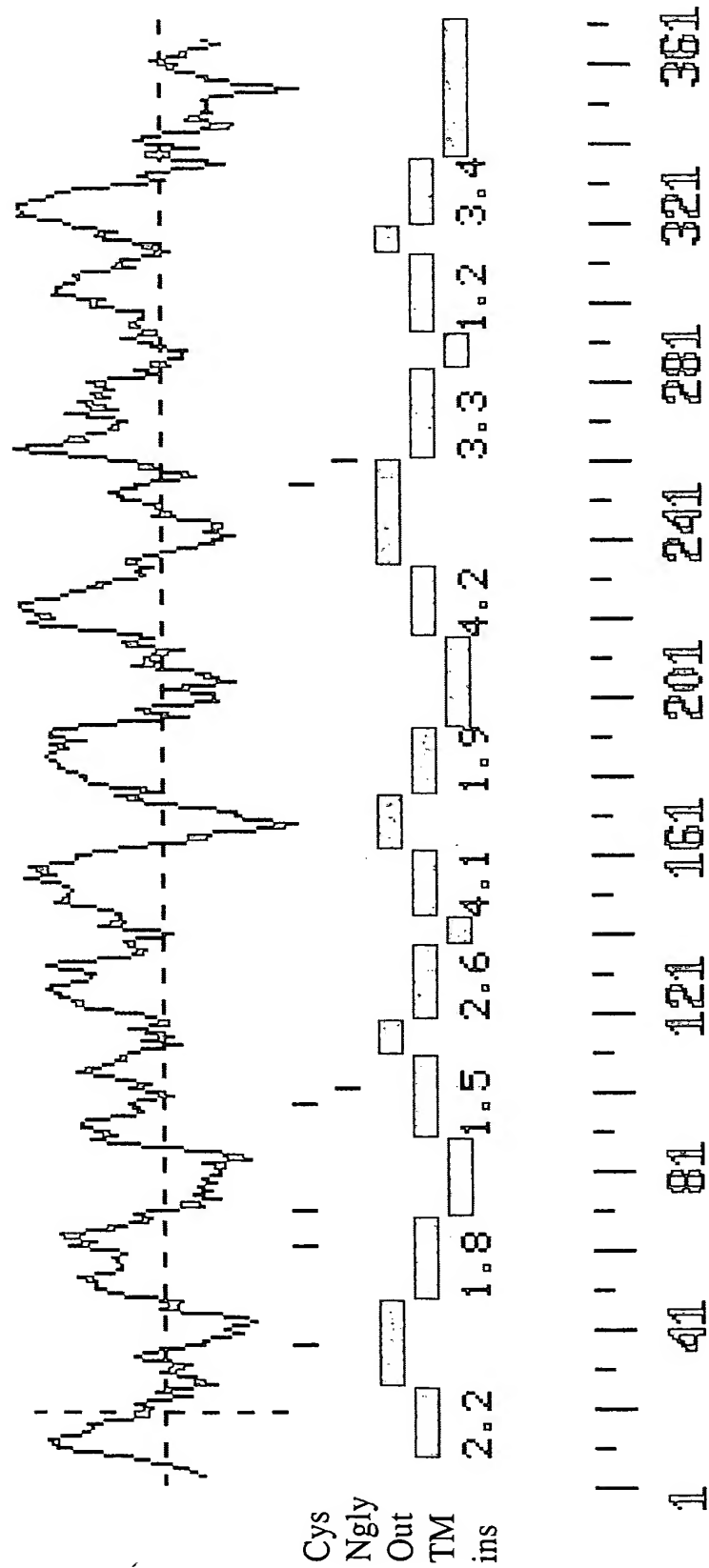


Fig. 20D

	M	A	P	H	W	
GTCGACCCACGCGTCCGGGACAGCTGGCCTGAAGCTCAGAGCCGGGGCGTGC GCC	ATG	GCC	CCA	CAC	TGG	5
						72
A V W L L A A R L W G L G I G A E V W W						25
GCT GTC TGG CTG CTG GCA AGG CTG TGG GGC CTG GGC ATT GGG GCT GAG GTG TGG TGG						132
N L V P R K T V S S G E L A T V V R R F						45
AAC CTT GTG CCG CGT AAG ACA GTG TCT TCT GGG GAG CTG GCC ACG GTA GTA CGG CGG TTC						192
S Q T G I Q D F L T L T L T E P T G L L						65
TCC CAG ACC GGC ATC CAG GAC TTC CTG ACA CTG ACG CTG ACG GAG CCC ACT GGG CTT CTG						252
Y V G A R E A L F A F S M E A L E L Q G						85
TAC GTG GGC GCC CGA GAG GAG GCC CTG TTT GCC TTC AGC ATG GAG GCC CTG GAG CTG CAA GGA						312
A I S W E A P V E K K T E C I Q K G K N						105
GCG ATC TCC TGG GAG GAG GCC CCC GTG GAG AAG AAG ACT GAG TGT ATC CAG AAA GGG AAG AAC						372
N Q T E C F N F I R F L Q P Y N A S H L						125
AAC CAG ACC GAG TGC TTC AAC TTC ATC CGC TTC CTG CAG CCC TAC AAT GCC TCC CAC CTG						432
Y V C G T Y A F Q P K C T Y V V S A A L						145
TAC GTC TGT GGC ACC TAC GCC TTC CAG CCC AAG TGC ACC TAC GTC GTG AGT GCT GCC CTC						492

Fig. 21A

L	P	R	C	P	P	Q	P	A	L	L	T	L	L	W	T	R	G	C	G	165
CTA	CCT	CGG	TGT	CCC	CAG	CCC	CCC	GCC	CTC	CTC	ACC	CTT	CTC	TGG	ACT	CGT	GGA	TGT	GGC	552
P	Q	S	P	A	L	K	H	L	L	I	T	S	L	S	V	L	R	T	C	185
CCA	CAG	AGC	CCT	GCC	CTT	AAG	CAT	CTC	CTC	ATC	ACC	TCT	CTC	TCT	GTC	CTT	AGA	ACA	TGC	612
S	P	S	L	W	S	M	E	S	L	K	M	G	R	A	S	V	P	M	T	205
TCA	CCT	TCA	CTT	TGG	AGC	ATG	GAG	AGT	TTG	AAG	ATG	GGA	AGG	GCA	AGT	GTC	CCT	ATG	ACC	672
Q	L	R	A	M	L	A	F	L	W	M	V	S	C	T	R	P	H	S	T	225
CAG	CTA	AGG	GCC	ATG	CTG	GCC	TTC	TTG	TGG	ATG	GTG	AGC	TGT	ACT	CGG	CCA	CAC	TCA	ACA	732
T	S	W	A	R	N	P	L	S	C	V	T	W	G	P	T	T	P	*		244
ACT	TCC	TGG	GCA	CGG	AAC	CCA	TTA	TCC	TGC	GTA	ACA	TGG	GGC	CCC	ACC	ACT	CCA	TGA		789
																				868
AGACAGAGTACCTGGCCCTTTTGGCTCAACGAACCTCACTTTGTAGGCTCTGCCCTATGTACCTGAGAGTGTGGCAGCTT																				
CACGGGGACGACGACAAGGTCCTACTTCTTTCAGGGAGCGGGCAGTGGAGTCCGACTGCTATGCCGAGCAGGTGGTG																				947
GCTCGTGTGGCCCGTGTCTGCAAGGGCGATATGGGGGGCGCACGGACCCCTGCAGAGGAAGTGGACCACGTTCCCTGAAGG																				1026
CGCGGCTGGCATGCTCTGCCCCGAACTGGCAGCTCTACTTCAACCAGCTGCAGGGCGATGCACACCCCTGCAGGACACCTC																				1105

Fig. 21B

CTGGCACAACACCTTCTTTGGGGTTTTCAAGCACAGTGGGTGACATGTACCTGTGCGCCATCTGTAGTACCAG 1184
TTGGAAGAGATCCAGCGGTGTTTGAGGGCCCCCTATAAGGAGTACCATGAGGAAGCCCCAGAAAGTGGGACCGCTACACTG 1263
ACCCTGTACCCAGGCCCTGGTTGTGATGGCTGCCCCAGCCCCGCAATGCCGGGCTACCACTGCTTTTCAGAGGAGCAG 1342
GGGGCGGGCTGGCTGCTGAAGCTACCTTGTGGCTGTCGTGGCAGGCCCGTCGGTGACCTTGAGGGCCCCGGCCCCCCC 1421
TGGAAAACCTGGGGCTGGTGTGGCTGGCGGTGGTGCCCCCTGGGGGCTGTGTGCCCTGGTGTGCTGCTGCTGGTGTCTGTC 1500
ATTGCGCCGGCGCTGCGGGAAGAGCTGGAGAAAAGGGCCAAAGGCTACTGAGAGGACCTTTGGTGTACCCCCCTGGAGCTG 1579
CCCAAGGAGCCCAACAGTCCCCCTTCCGGCCCCCTGTCCTGAAACCAGATGAGAAAACTTTGGGATCCTGTGCGTTACTACT 1658
ATTCAGATGGCTCCCTTAAGATAGTACCTGGGCATGCCCCGGTGCCAGCCCCGGTGGGGGGCCCCCTTCGCCACCTCCAGG 1737
CATCCCAGGCCAGCCTCTGCCCTTCTCCAACCTCGGCTTCACCTGGGGGGGTGGGCGGGAACCTCAAATGCCAAATGGTTACGTG 1816
CGCTTACAAC TAGGAGGGAGGACCGGGGAGGGCTCGGGGCACCCCCCTGCCCTGAGCTCGCGGATGAAC TGAAGACGCAAAC 1895
TGCAGCAACGCCAGCCACTGCCCGACTCCAACCCCGAGGAGTCATCAGTATGAGGGGAACCCCCACCCGCTCGGCGGGA 1974
AGCGTGGAGGTAGCTCCTACTTTTGACACAGGCACCAAGCTACCTCAGGGACATGGCACGGGCACCTGCTCTGTCTGG 2053

Fig. 21C

GACAGATACTGCCCCAGCACCCACCCGGCCATGAGGACCTGCTCTGCTCAGCACGGGCACCTGCCACTTGGTGTGGCTCAC 2132
CAGGGCACCCAGCCCTCGCAGAAAGGCATCTTCCCTCCTCTCTGTGAATCACAGACACGCGGGACCCAGCCGCCAAAACTTT 2211
TCAAGGCAGAAAGTTTCAAGATGTGTGTTTTGTCTGTATTTGCACATGTGTTTTGTGTGTGTATGTGTGTGTGCACGC 2290
GCGTGGCGCCTTGTGGCATAGCCCTTCCGTGTTTTCTGTCAAAGTCTTCCCTTGGCCCTGGGTCCCTCGGTGAGTCATTGGAG 2369
CTATGAAGGGGAAGGGTCCGTATCACTTTTGTCTCTCTACCCCCACTGCCCCGAGTGTGCGGCAGCGATGTACATATGG 2448
AGGTGGGTGGACAGGGTGTGTGCCCCCTTCAGAGGGAGTGCAGGGCTTGGGGTGGGCCCTAGTCCTGCTCCTAGGGCTG 2527
TGAAATGTTTTACAGGTGGGGGAGGAGATGGAGCCCTCCTGTGTGTTTTGGGGGGAAGGTTGGGTGGGGCCCTCCCACTTG 2606
GCCCCGGGTTCAGTGGTATTTTATACTTGCCCTTCTTCCGTACAGGGCTGGGAAAGGCTGTGTGAGGGGAGAGAAGGG 2685
AGAGGGTGGCCCTGCTGTGGACAATGGCATACTCTCTTCCAGCCCTAGGAGGGGCTCCTAACAGTGTAACCTTATTGT 2764
GTCCCCGCGTATTATTGTTGTAAATATTTGAGATTTTATATTGA 2811

Fig. 21D

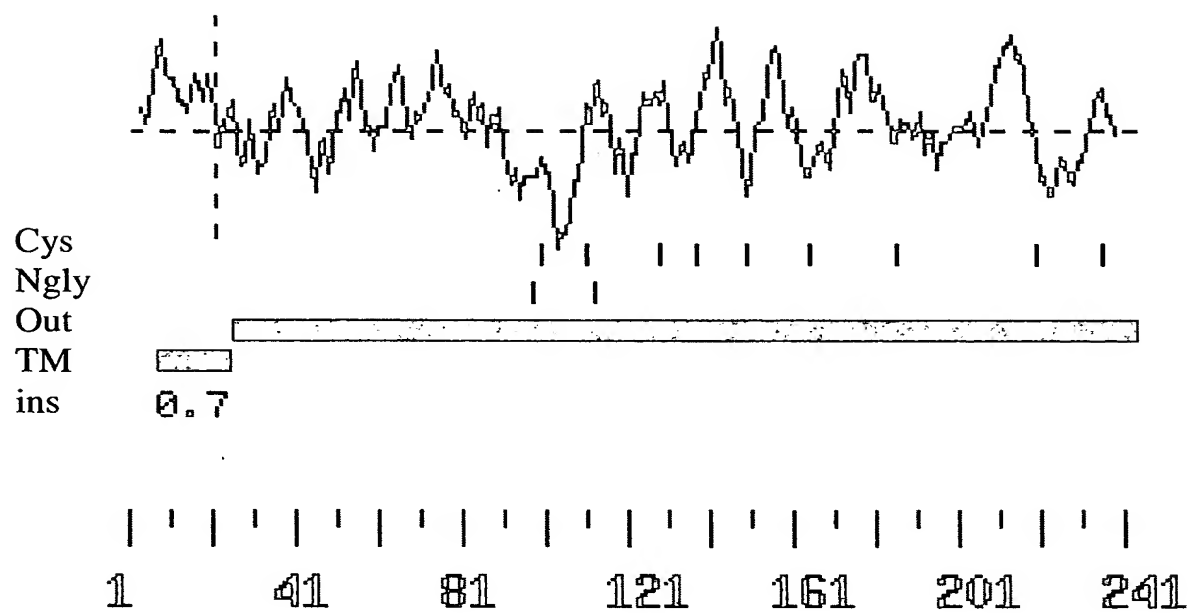


Fig. 21E


```

360      370      380      390      400      410      420
M QAQKWAYRTDPVSPRPGSCINNWHRDNGYTSSLELPDNTLNFIKKHPLMEDQVKPRLGRPLLVKKNTNF
  ::      ::      ::      ::      ::      ::      ::
H ---WTR-----GCGPQ-----SPAL-----KH-----LLI-----TSL
160                                     170

430      440      450      460      470      480      490
M THVVADRVPGLDGATYTVLFIGTGDGWLKAVSLGPWIHMVEELQVFDQEPVESLVSQSKKVLFAGSRS
  .      .      .      .      .      .      .
H S-----VLRTCSPSLW-----SMESLKMGRA-----SVPMT
180                                     190      200

500      510      520      530      540      550      560
M QLVQLSLADCTKYRFCVDCVLARDPYCAWNVNTSRCVATTSGRSGSFLVQHVANLDTSKMCNQYGIKKVR
  ::      ::      :      :      :      :      :
H QLRAM-LA-----F-----L-----WMVSCTRPHSTTS-----
210                                     220

570      580      590      600      610      620      630
M SIPKNITVSGTDLVLPCHLSSNLAAHAWTFGSQDLPAEQPGSFLYDTGLQALVVMAAQSRHSGPYRCYS
  :
H -----W-----

640      650      660      670      680      690      700
M EEQGTRLAESYLVAVAGSSVTLEARAPLENLGLVWLAVVALGAVCLVLLLVLSLRRRLREELEKGAK
  ::      ::      ::      ::      ::
H -----ARNPLS-----CVT-----
230

```

Fig. 21G

```

710      720      730      740      750      760      770
M ASERTLVYPLELPKEPASPFRPGPETDEKLWDVPVGYYSYSDGSLKIVPGHARCQPGGGPPSPPPGIPGQP
H -----W-----GPTTP-----
      :
      :: ::
      240

780      790      800      810      820      830
M LPSPTRLHLGGGRNSNANGYVRLQLGGEDRGSGHPLPELADELRRKLQQRQLPDSNPRESSV
H -----

```

Fig. 21H

```

10      20      30      40      50      60      70
M  GGCACGAGGTGGCCGGAGTCAAAACGCGAGGCGCAGCCAGGGATTGGAGCTGCACGAAAGAGGGCTGCTG
:  :      :      :      :      :      :      :      :      :      :      :
H  GTC-----GACC-----CACG-----CGTC-----CGCG-----GGACAGCTG
10      20

80      90      100     110     120     130     140
M  GACTGAAGTTAGACCCTGGGTGCTGCCATGGCCCCACACTGGGCTGTCTGGCTGCTGGCAGCAGGGCT
:  :      :      :      :      :      :      :      :      :      :      :
H  GCCTGAAGCTCAGAGCCGGGCGTGCGCCATGGCCCCACACTGGGCTGTCTGGCTGCTGGCAGCAAGGCT
30     40     50     60     70     80     90

150     160     170     180     190     200     210
M  GTGGGGCCCTGGGCATCGGGGCTGAGATGTGGTGAACCTTGTGCCCGGAAGACAGTATCTTCTGGGAG
:  :      :      :      :      :      :      :      :      :      :      :
H  GTGGGGCCCTGGGCATTTGGGCTGAGGTGTGGTGAACCTTGTGCCCGGTAAGACAGTGTCTTCTGGGAG
100    110    120    130    140    150    160

220     230     240     250     260     270     280
M  CTGGTCACAGTAGTGAGGCGGTTCTCCAGACAGGCATCCAGGACTTCCTGACACTGACCCCTGACAGAAC
:  :      :      :      :      :      :      :      :      :      :      :
H  CTGGCCACGGTAGTACGGCGGTTCTCCAGACCGGCATCCAGGACTTCCTGACACTGACGCTGACGGAGC
170    180    190    200    210    220    230

290     300     310     320     330     340     350
M  ATTCTGGCCCTTTATATGTGGGGGCCCCGAGAGGCGCTGTTTGCCCTTCAGTGTAGAGGCTCTGGAGCTGCA
:  :      :      :      :      :      :      :      :      :      :      :
H  CCACTGGGCTTCTGTACGTGGGCGCCCCGAGAGGCCCTGTTTGCCCTTCAGCATGGAGGCCCTGGAGCTGCA
240    250    260    270    280    290    300

```

Fig. 21I


```

710      720      730      740      750      760      770
M TCAAGACAGAGTACCTGGCTTTTGGCTGAATGAACCCACACTTTGTAGGCTCTGCCCTTTGTCCCTGAGAG
  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::
H -----AGAGCCCTGCCCTTAAGC-----ATCTCCTCATCAC---CTCTCTCTCTGTCC-TTAGA-
560      570      580      590      600

780      790      800      810      820      830      840
M TGTGGGAAGCTTCACGGGAGACGATGACAAGATCTACTTCTTCTTCAGTGAGCGGCGAGTGGAGTATGAC
  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::
H -----ACATGCTCACCTTCA-CTT-TG-GAGCA---TGGAGAGTTTGA-
610      620      630      640

850      860      870      880      890      900      910
M TGCTATCCGAGCAGGTGGTGGCTCGTGTGGCGAGAGTCTGTAAGGTGACATGGGGGAGCACGGACGC
  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::
H -----AGATGG-----GAAGGGCAAGTGTG-----C-----CTATGACCC
650      660      670

920      930      940      950      960      970      980
M TGCAGAAATAATGGACGACGTTCCCTGAAGGCTCGGTTGGTGTGCTCAGCCCCCTGACTGGAAGGTCTACTT
  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::
H AGCTAAGGGCCATGCTGGCCCTTCTTGT-GGATGGTGAGCTGTACTCGGCCAC--ACT-----CAACAA
680      690      700      710      720      730

990      1000     1010     1020     1030     1040     1050
M CAACCAGCTGAAGCGGTGCACACCCCTGCGGGGCGCCTCTTTGGCACAAACACCACCTTCTTCGGGGTTTTT
  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::
H CTTCCCTG-----GGCA-----CGGAAC-CCA-TTATC-----CTGCG-----TAA
740      750      760

```

Fig. 21K

```

1060      1070      1080      1090      1100      1110      1120
M CAAGCGGATGGGGCGATATGGACCTGTCTGCAGTTTGTGAGTACCAGTTGGAACAGATCCAGCAAGTGT
::      :::::      ::      :      ::::      :      ::::
H CA-----TGGGGC-----CC--C-----ACCA-----C---TCCA-----
770                                780

1130      1140      1150      1160      1170      1180      1190
M TTGAGGGTCCCTACAAGGAGTACAGTGAGCAAGCCAGAAAGTGGCCCGCTATACTGACCCGGTACCCAG
:::::      ::      :::::      :::::      .. ::::      :      :      :      :      :
H -TGAAG-----ACA--GAGTAC-----CTGGCC---TTTGGCTCAACGAACCTCACTTTGTA---GG
790                                800      810      820      830

1200      1210      1220      1230      1240      1250      1260
M CCCTCGGCCTGGTTTCGTGTATCAACAACCTGGCACCGAGACAATGGCTACACCAGTTCCCTGGAACGTCCG
:      ::      :::::      :      ::::      .. :::::      :      :      :      :      :
H C--TCTGCCTA-----TGTA-C-----CTGA-----GAGT-GTGGGCAGCTTCA---CGGGGACGAC--
840                                850      860      870      880

1270      1280      1290      1300      1310      1320      1330
M GACAACACCCCTCAACTTCATCAAGAAGCACCCCTGATGGAGGACCAGGTGAAGCCTCGGTTGGGCCGCC
:::::      :      :      :::::      :::::      ::::      :      :      :      :      :
H GACAAGGTCTACTTCTTCTTCAGGGAGC-----GGGC--AGTGGAGTC-CGA-----
890      900      910      920

1340      1350      1360      1370      1380      1390      1400
M CCTACTTGTGAAGAAGAACACTAACTTCACACACGTGGTGGCCGACAGGGTCCCAGGGCTTGATGGTGC
:::::      ::      :      ::      :::::      ::      :      :      :      :      :
H --CTGCTA-----TGC--CGAGCAGGTGGTGGC-----TC-----GTGTGGC
930                                940      950

```

Fig. 21L

```

1410      1420      1430      1440      1450      1460      1470
M CACCTATACAGTGTGTTTCATTGGTACAGGAGATGGCTGGCTGCTGAAGCTGTGAGCCCTGGGCCCCCTGG
: . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H C--CGTGTCTG-----CAAGGG--C--GATATGGGGGC-----GCA-----C--GGACCCCTG-
960      970      980      990

1480      1490      1500      1510      1520      1530      1540
M ATCCACATGGTGGAGGAACTGCAGGTGTTTGACCAAGGAGCCAGTGGAAGTCTGGTGTCTCTCAGAGCA
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H -----GAGGAA-----GTG-----GACCACGTTCCCTG-----AAGGC-----GCGG-----CTG-GCA
1000      1010      1020      1030

1550      1560      1570      1580      1590      1600      1610
M AGAAGGTGCTCTTTGCTGGCTCCCGCTCTCAGCTGGTTTCAGCTGTCTCTGGCCGACTGCACAAAGTACCG
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H -----TGCTCT-----GC-CCCGAACT-GGCAG-CTCTACT-TCA---ACCAGCTGCA---GG---CG
1040      1050      1060      1070      1080

1620      1630      1640      1650      1660      1670      1680
M TTTCTGTAGACTGTGTCTCTGGCCAGGAGCCCTTACTGTGCCCTGGAATGTCAACACCAGCCGCTGTGTG
. : . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H ATGC-----ACA---CCCTG--CAGGACACCT-----CCTGGCA---CAACACCACCTTCTTTTGGG
1090      1100      1110      1120      1130

1690      1700      1710      1720      1730      1740      1750
M GCCACCACCAAGTGGTCGCTCGGGGTCCCTTCTGTGTCACACATGTGGCGAACTTGGACACTTCAAAGATGT
: . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H GTTT--TTCAA-----GCACAGTGG-----GGT--GACATGTACCTGTC---GGC-CATCTG---TGA
1140      1150      1160      1170

```

Fig. 21M

```

1760      1770      1780      1790      1800      1810      1820
M  GTAACCAAGTATGGCAATTAAAAAGTCAGATCTATTCCCAAGAACATCACCGTTGTGTCAAGGCACAGACCT
   ::::: ::::: ::::: ::::: ::::: ::::: :::::
H  GTA-CCAGT-TGG-----AAG--AGATC-----CAGCG--GGTGTTTGAGG-----
1180      1190      1200      1210

1830      1840      1850      1860      1870      1880      1890
M  GGTCCTACCCCTGCCACCTCTCGTCCAATTGGCCCATGCCCACTGGACCTTCGGAAGCCAGGACCTGCCT
   ::::: ::::: ::::: ::::: ::::: ::::: :::::
H  -----GCC-----CCTATAAGGA--GTACC--ATGA-----GGAAGC-----CCA
1220      1230      1240

1900      1910      1920      1930      1940      1950      1960
M  GCAGAACCAACCTGGCTCCTTTCTTATGACACGGGACTCCAGGCGCTGGTGGTATGCCCCGACAGTCCC
   : ::::: ::::: ::::: ::::: ::::: ::::: :::::
H  GAAGTGGGACC--GCTAC--ACT---GACCCCTGTAC-CCAGGCCCTGGTGTGTGATGGCTGCCCAAGCCCCC
1250      1260      1270      1280      1290      1300

1970      1980      1990      2000      2010      2020      2030
M  GTCACCTCTGGACCCCTATCGTTGCTATTTCAGAGGAGCAGGGGACAAAGACTGGCTGCAGAAAGCTACCTTGT
   : : : ::::: ::::: ::::: ::::: ::::: ::::: :::::
H  GCCATGCCGGGGCCTACCACTGCTTTTCAGAGGAGCAGGGGGCGCGGCTGGCTGCTGAAGGCTACCTTGT
1310      1320      1330      1340      1350      1360      1370

2040      2050      2060      2070      2080      2090      2100
M  TGCTGTCTGGCCGGCTCGTCTGGTGACACTGGAGGCACGGGCTCCCTTGGAAAAACCTGGGGCTCGTGTGG
   ::::: ::::: ::::: ::::: ::::: ::::: :::::
H  GGCTGTCTGGCAGGCCCGTCTGGTGACCTTGGAGGCCCGGGCCCCCTGGAAAAACCTGGGGCTGGTGTGG
1380      1390      1400      1410      1420      1430      1440

```

Fig. 21N

[illegible]

Fig. 210

```

2460      2470      2480      2490      2500      2510      2520
M CTCAAATGCCAATGGTTATGTGCGTTTACAGTTGGCGGAGAGAGACCAGAGGATCTGGGCACCCACTG
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H CTCAAATGCCAATGGTTACGTGCGCTTACAACCTAGGAGGGAGGACCGGGAGGGCTCGGGCACCCCTG
1800      1810      1820      1830      1840      1850      1860

2530      2540      2550      2560      2570      2580      2590
M CCTGAGCTCGCGGATGAATTACGACGGAACTACAACAGCCAGCCGCTGCCCTGACTCCAACCCAGAGG
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H CCTGAGCTCGCGGATGAACCTGAGACGCAAACTGCAGCAACGCCAGCCACTGCCCGACTCCAACCCCGAGG
1870      1880      1890      1900      1910      1920      1930

2600      2610      2620      2630      2640      2650
M AGTCCTCAGTATGAGGGACCCCCCACCCTCATTTGGCGGGGGGTCTCATGGGAGGTGCA-CTCTTAA
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H AGTCATCAGTATGAGGGGAACCCCC-ACCGCGTCGGCGGGAAG-----CGTGGAGGTGTAGCTCCTA-
1940      1950      1960      1970      1980      1990

2660      2670      2680      2690      2700      2710      2720
M CTTTGCACAGGCACCACTACCTCAGGGACATGGCAGGGGCACTTGCTCTGCCCTGGGACAGACACTGCC
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H CTTTGCACAGGCACCACTACCTCAGGGACATGGCAGGGCACTGCTCTGTCTGGGACAGATACTGCC
2000      2010      2020      2030      2040      2050      2060

2730      2740      2750      2760      2770      2780      2790
M CATCATTTGCCCCGGCGTGAGGACCTGCTC-----AGCATGGGCACTGCCACTTGGTGTGGCTCACCAGG
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H CAGCACCCACCCGGCCATGAGGACCTGCTCTGCTCAGCACGGGCACTGCCACTTGGTGTGGCTCACCAGG
2070      2080      2090      2100      2110      2120      2130

```

Fig. 21P

```

2800      2810      2820      2830      2840      2850      2860
M ACTTCAGCCTCACAGGAGACA-CACCCCTCCTCT--GTGAATTGAGACATGTGGGACCCAGCAGCCAAA
.. : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H GCACCAAGCCTCGCAGAAGGCATCTTCCTCCTCTCTGTGAATCACAGACACGCGGACCCAGCCGCCAAA
2140      2150      2160      2170      2180      2190      2200

2870      2880      2890      2900      2910      2920
M ACTTTGCAAGGAAGAGGTTTCAAGATGTGGCGTGTTTGTGCAT--ATATGTGTTGGTATGCATGTGGAA
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H ACTTTTCAAGGCAGAGTTTCAAGATGTGTGTTTGTCTGTATTTGCACATGTGTTTGTGTGTGTGTAT
2210      2220      2230      2240      2250      2260      2270

2930      2940      2950      2960      2970      2980      2990
M GAATGTGTGTGTGTGTGTG---TGTTGTGTAACTTTCCTGTCTCTATCACGTCTTCCCTTGGCCTGG
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H GTGTGTGTGCACGCGGTGCGCGCTTGTGGCATAGCCTTCCCTGTTCCTGTCTGTCAAGTCTTCCCTTGGCCTGG
2280      2290      2300      2310      2320      2330      2340

3000      3010      3020      3030      3040      3050      3060
M GGTCCCTCCCTGGTTGAGTCTTTGGAGCTATGAAGGGAAGGGGTCTATAGCACTTTGCTTCTCCTACCCCC
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H G-TCCCTCCCTGGT-GAGTCATTGGAGCTATGAAGGGAAGGGG-TCGTATCACTTTGTCTCTCCTACCCCC
2350      2360      2370      2380      2390      2400      2410

3070      3080      3090      3100      3110      3120      3130
M AGCTGTCCCAAGCTTTGGGGCAGTGATGTACATACGGGGAAGGAAGGACAGGGTGTGTACCCCTTTTG
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H A-CTGCCCCCGAG-TGTCGGGCACCGATGTACATATGGAGGTGGGTGGACAGGGTGTGTGCCCCCTTCAG
2420      2430      2440      2450      2460      2470      2480

```

Fig. 21Q

```

3140      3150      3160      3170      3180      3190      3200
M GGGAGTGGGGACTCGGGGTGGGCCCTAGCCCTGCTCCTAGGGCTGTGAATGTTTTCAGGGCGGGGTT
.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.
H AGGAGTGCAGGGCT-TGGGGTGGGCCCTAGTCCCTGCTCCTAGGGCTGTGAATGTTTTCAGGGTGGGGGA
2490      2500      2510      2520      2530      2540      2550

3210      3220      3230      3240      3250      3260      3270
M GGGGTGGAGATGGAACCTCCTGC---TTCAGGGGAGGGGTGGGCAGGGCCTCCCACTTGCCCTCCGGG
.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.
H GGG-----AGATGGAGCCTCCTGTGTGTTTGGGGGAAGGTGGTGGGCCCTCCCACTTGCCCGGGG
2560      2570      2580      2590      2600      2610

3280      3290      3300      3310      3320      3330
M TTCGGTGGTATTTATATTGCGCTCTTC-TG-ACAGGCTGGGAAGG--TTGTTGGGGAGGAAGGG
.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.
H TTCAGTGGTATTTATACTTGCCTTCTTCCTGTACAGGCTGGGAAGGCTGTGTGAGGGAGAGAAGGG
2620      2630      2640      2650      2660      2670      2680

3340      3350      3360      3370      3380      3390      3400
M AGGAGGTGGGCATGCTATGGATACTGGCCCTATCCTCTCCCTGCTCTGGGAAAAGGCT---AACAGTGA
.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.
H AGAGGGTGGGCCCTGCTGTGGACAATGGCATACTCTCTTCCAGCCCTAGGAGGAGGCTCCTAACAGTGA
2690      2700      2710      2720      2730      2740      2750

3410      3420      3430      3440      3450      3460      3470
M ACTTATTGTGTCCCCACATATTATTGTTGTAAATATTGAGTATTTTATATTGACAAAATAAATGGA
.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.
H ACTTATTGTGTCCCCCGTATTATTGTTGTAAATATTGAG-ATTTTATATTGA-----
2760      2770      2780      2790      2800      2810

```

Fig. 21R

GTCGACCCACGCGTCCGCGGACGCGTGGCGCGCGGGGCCCATCCAGACCCCTGCGGAGAGCGGCCCGGAGCGTCGCC	79
GAGGTTGAGGCGCGGAGACCGAGGCGCTGGCGGCCGGAAGAACCGCCCCAAGAAGAGCCTCTGGCCCCGGGGGCTGC	158
<div style="display: flex; justify-content: space-around; margin-bottom: 5px;"> MFTLLVLL </div> TGGAACATGTGCGGGGGACACAGTTTGTGACAGTTGCCAGACT ATG TTT ACG CTT CTG GTT CTA CTC	8 228
<div style="display: flex; justify-content: space-around; margin-bottom: 5px;"> SQLPTVTLGFPHCARGPKAS </div> AGC CAA CTG CCC ACA GTT ACC CTG GGG TTT CCT CAT TGC GCA AGA GGT CCA AAG GCT TCT	28 288
<div style="display: flex; justify-content: space-around; margin-bottom: 5px;"> KHAGEEVFTSKEEANFFIHR </div> AAG CAT GCG GGA GAA GAA GTG TTT ACA TCA AAA GAA GAA GCA AAC TTT TTC ATA CAT AGA	48 348
<div style="display: flex; justify-content: space-around; margin-bottom: 5px;"> RLLYNRFDLELFTPGNLERE </div> CGC CTT CTG TAT AAT AGA TTT GAT CTG GAG CTC TTC ACT CCC GGC AAC CTA GAA AGA GAG	68 408
<div style="display: flex; justify-content: space-around; margin-bottom: 5px;"> CNEELCNYEEAREIFVDEDK </div> TGC AAT GAA GAA CTT TGC AAT TAT GAG GAA GCC AGA GAG ATT TTT GTG GAT GAA GAT AAA	88 468
<div style="display: flex; justify-content: space-around; margin-bottom: 5px;"> TIAFWQEYSAKGPTTKSDGN </div> ACG ATT GCA TTT TGG CAG GAA TAT TCA GCT AAA GGA CCA ACC ACA AAA TCA GAT GGC AAC	108 528

Fig. 22A

R	E	K	I	D	V	M	G	L	L	L	T	G	L	I	A	A	G	V	F	L	128
AGA	GAG	AAA	ATA	GAT	GTT	ATG	GGC	CTT	CTG	ACT	GGA	TTA	ATT	GCT	GCT	GGA	GTA	TTT	TTG	588	
V	I	F	G	L	L	G	Y	Y	L	C	I	T	K	C	N	R	L	Q	H	148	
GTT	ATT	TTT	GGA	TTA	CTT	GGC	TAC	TAT	CTT	TGT	ATC	ACT	AAG	TGT	AAT	AGG	CTA	CAA	CAT	648	
P	C	S	S	A	V	Y	E	R	G	R	H	T	P	S	I	I	F	R	R	168	
CCA	TGC	TCT	TCA	GCC	GTC	TAT	GAA	AGG	GGG	AGG	CAC	ACT	CCC	TCC	ATC	ATT	TTC	AGA	AGA	708	
P	E	E	A	A	L	S	P	L	P	P	S	V	E	D	A	G	L	P	S	188	
CCT	GAG	GAG	GCT	GCC	TTG	TCT	CCA	TTG	CCG	CCT	TCT	GTG	GAG	GAT	GCA	GGA	TTA	CCT	TCT	768	
Y	E	Q	A	V	A	L	T	R	K	H	S	V	S	P	P	P	P	Y	P	208	
TAT	GAA	CAG	GCA	GTG	GCG	CTG	ACC	AGA	AAA	CAC	AGT	GTT	TCA	CCA	CCA	CCA	TAT	CCT	828		
G	H	T	K	G	F	R	V	F	K	K	S	M	S	L	P	S	H	*		227	
GGG	CAC	ACA	AAA	GGA	TTT	AGG	GTA	TTT	AAA	AAA	TCT	ATG	TCT	TCT	CTC	CCA	TCT	CAC	TGA	885	
CTACCT	TGTCAT	TTTGGT	ATAAGAAA	TTTGTG	TTATT	TGATAG	CGCGGCAT	GGTGGCTCAT	GCCTGTAA	TCCCAGCAC										964	
TTTGGG	AGGCCAGG	AGTTCG	AGACCAG	CCTGG	CCACAT	GGTGAA	ACCCGGTCTCTACT	AAAAATTCA	AAAAATTACCTA	1043											
GGCGT	CATGGGG	CATGCC	TGTAGT	CCCCAC	CTACTT	GGGAGG	CTGAAG	CAGAGA	ATTGCT	CGAACCT	GGGAGG	CAGAGG	1122								

Fig. 22B

TTGCAGTAAGCTGAGATCACGCCACTGCAATCCAGCCTGGCGGACAGAGCAAGACTCCATCTCAAAAAATAAAATAAAAA 1201
 AAGAAAGAAAAGAAAGAAAAGAAAGAAAGGAGATGAAAGGAGGAGGAGGAGAGAGAAAGAGAA 1280
 GAAGAAGAAGACCACAAAAGACATGACTATCCAACTTTTATGACAAACTGCAAGGAAATAAAGGAAATAAGTCCATG 1359
 TACTGTACCACAGAAGTCTGTCTGCATCTTGGACCTGAACTTGATCATATCAGCTTGATAAGAGACTTTTGTGACTCT 1438
 ATATCCTTGCAGTTAAGAAGAAAAGCACCTTTTGTAAATGTTTAAATGGTTCAAAAAAATCTTCTTATAAAAGAG 1517
 CATAGGTAGAAATTAGTGAACCTCTTTGGATCCTTTGTACAGATAAAGTTATAGATTTCCTTGTGTTGAATATTAAAAAAG 1596
 CAAGGATGCTTAACCATTAAGATTATCCAAAGTCAGGCTGGGCGCAGTGGCTCACGCCGTGTAATCCAGCACCTTTGGGA 1675
 GGGATAGGTGGCGGATCACCTGAGGTCAGGAGTTTGAGACCAGCCTGGCCAAACATGGCAAAACCCCGTCTCTACAAAA 1754
 ATACAAAAGAAATTAGCCAGACATGATGGCGGTGCCTCTAAATCCAGCTACTGGGAGGCTGAGGTGGAGAAATCGCT 1833
 TGAACCTCGGAGGTGGAGGTGTAGTGAGGCGAGATTGTGCCATTGCACTCCAACTGGGCGACAGAGTGAGACTCCAT 1912
 CTCAAAAAATAAAAAAAGATTATCCAAAAAGATATTGGACCTACTCTTTCTTAGGATTTTGTGGCGGGGT 1991
 TAGAAATACCTCACAGAAATTGACATTTGACATATTCAGTATAAAATCTGTGACCTTAATAATAATCACTTGGTTTATATGTTAAATT 2070
 ATTGCACACAGTCATCATATTTTGCAGAGTTTAGTCTTAACTCTTGCTGTCAGTCATGTTTATATATAGGTAGTGG 2149
 GTCAGTAGTTTCTCTCTAAAAAATACATATTGCTATGAAGTTAGTTCTTTCAGAAAGATACAAGTTTGCAATGAAAAAG 2228
 GATTTGCAAGGGTTGTTATGCTATCAAAATAAACAGACCCTAAAACTAGGAGACACTAGAACTTAATGAAGTGCCTG 2307
 TTACTGATTAGTAAATACTCCCATCTTCGTTGCAAAAATTATCTCTCTGTATAACTACATATGATTATTTGAAAAATTGT 2386
 TAAACTTCATAAGTAATAGTTTGAGAAATGTGGAAAAAGTAATTGTCTTTTCTGCTCTTAAAAATAATATTGATTAAATGTT 2465
 ACCAGAAAAAATAAAAAAAGGGCGCGC 2498

Fig. 22C

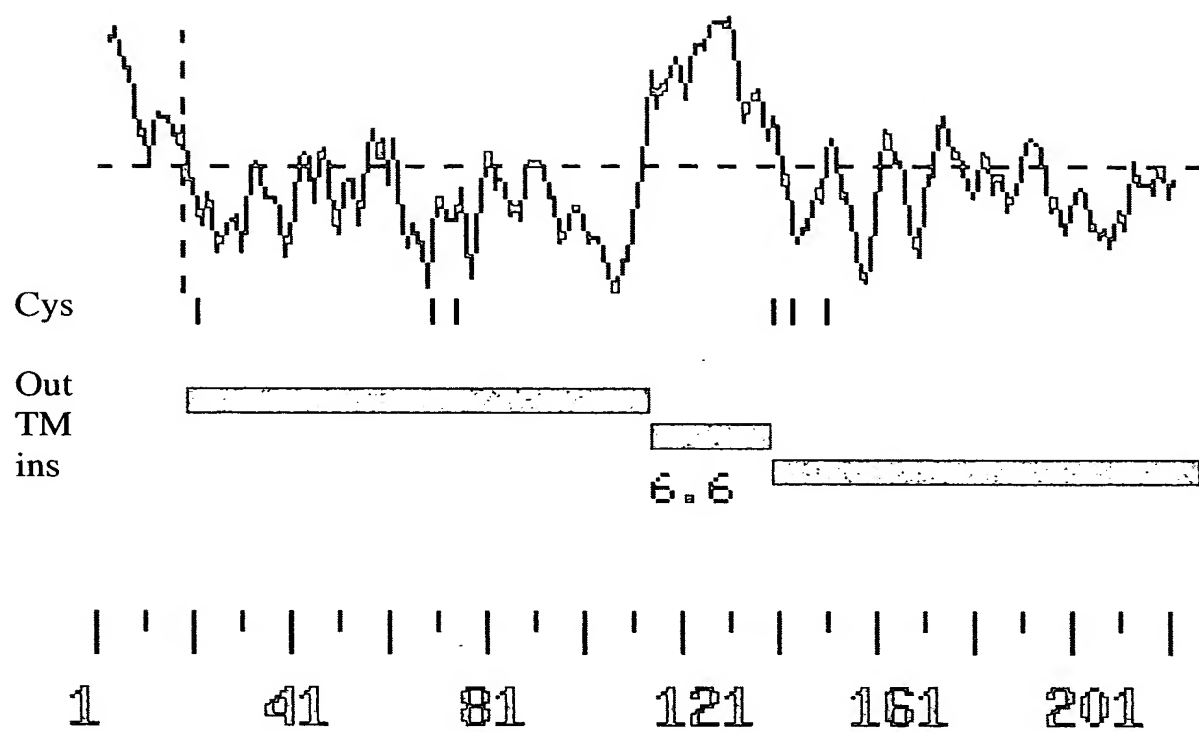


Fig. 22D

GTCGACCCAC	CGGTCCGCTG	CGTTCTCACC	CCTGGACCAC	CCTGGGAGAA	CAGTTGACCG	60
AAGTTTGTTT	GGCAGTTGCT	GCTGGACT	ATG TTT CTG	CTT CTG	GTG GTA CTC	112
	Met	Phe	Leu	Leu	Val Val Leu	
	1			5		
AGC CAG CTG	CCC AGA CTT	ACC CTC	GCG GTT	CCT CAT	ACA AGA AGC CTA	160
Ser Gln Leu	Pro Arg Leu	Thr Leu	Ala Val	Pro His	Thr Arg Ser Leu	
	10		15		20	
AAG AAT TCT	GAA CAT GCC	CCA GAA	GGA GTC	TTT GCA	TCA AAA AAA GCA	208
Lys Asn Ser	Glu His Ala	Pro Glu	Gly Val	Phe Ala	Ser Lys Lys Ala	
	25		30		35	
GCA AGC ATC	TTT ATG CAC	CGT CGC	CTC CTA	TAC Tyr	Asn Arg Phe Asp Leu	256
Ala Ser Ile	Phe Met	His Arg	Leu Leu	50	55	
	45					
GAA CTC TTC	ACT CCC	GGG AAC	CTG GAG	AGA GAG	TGC TAT GAG GAG TTC	304
Glu Leu Phe	Thr Pro	Gly Asn	Leu Glu	Arg Glu	Cys Tyr Glu Glu Phe	
	60		65		70	
TGT AGT TAT	GAA GAA	GCC AGA	GAG ATC	CTC GGG	GAC AAC GAA GAA ATG	352
Cys Ser Tyr	Glu Glu	Ala Arg	Glu Glu	Ile Leu	Gly Asp Asn Glu Glu Met	
	75		80		85	

Fig. 22E

ATC ACA TTC TGG CGG GAA TAT TCA GTC AAA GGA CCA ACC ACA AGA TCA	400
Ile Thr Phe Trp Arg Glu Tyr Ser Val Lys Gly Pro Thr Thr Arg Ser	
90 95 100	
GAT GTC AAC AAA GAG AAA ATT GAT GTT ATG GGC CTT CTG ACT GGC TTA	448
Asp Val Asn Lys Glu Lys Ile Asp Val Met Gly Leu Thr Gly Leu	
105 110 115 120	
ATT GCG GCT GGA GTA TTC TTG GTT GTT TTT GGC TTA CTT GGT TAC TAT	496
Ile Ala Ala Gly Val Phe Leu Val Val Phe Gly Leu Leu Gly Tyr Tyr	
125 130 135	
CTG TGT ATC ACC AAG TGT AAT AGG CAG CCA TAT CAA GGT TCT TCA GCT	544
Leu Cys Ile Thr Lys Cys Asn Arg Gln Pro Tyr Gln Gly Ser Ser Ala	
140 145 150	
GTC TAC ACA AGA AGG ACC AGG CAC ACA CCG TCC ATC ATT TTC AGA ACC	592
Val Tyr Thr Arg Arg Thr Arg His Thr Pro Ser Ile Ile Phe Arg Thr	
155 160 165	
CAT GAG GAA GCT GTC TTG TCT CCA TCG TCA TCC TCA GAG GAC GCG GGA	640
His Glu Glu Ala Val Val Ser Pro Ser Ser Ser Ser Glu Asp Ala Gly	
170 175 180	

Fig. 22F

CTA CCT TCC TAT GAA CAG GCA GTA GCT CTG ACC AGA AAA CAC AGT GTC	688
Leu Pro Ser Tyr Glu Gln Ala Val Ala Leu Thr Arg Lys His Ser Val	200
185	190
	195
TCA CCA CCA CCT CCA TAT CCT GGG CCA GCA AAA GGA TTT AGG GTA TTT	736
Ser Pro Pro Pro Pro Tyr Pro Gly Pro Ala Lys Gly Phe Arg Val Phe	215
	205
	210
AAA AAG TCA ATG TCA CTC CCA TCT CAC TAAGCCCACC TTGCCGCCCTT	783
Lys Lys Ser Met Ser Leu Pro Ser His	225
	220
GCTGTGGTCT GAATAATATG TTCTTCCTGA AACAAACAACA ACAAATAAAT TTGCCCTGTTT	843
AGCTTTTAT GACAAAGCAC AAGGAATAAAA GGAACACTAT ATACAGAACA GAATTCACCA	903
CAGCCCCGCT TTCAGCTCTG CCCCCAACTG GATTGCTGTC TTGGTAAGAG ACTTCTACCG	963
TGCTTCCTCG AAGTTAAGAA GAAAGTGCCT TTTTGCAATG TAAACTGTAC TGGTTCAAAC	1023
ATTCTTGCTA CAGCTAGGTA CCTATAATCC CCACCTTCAG GAGACTTAGG CGGAGGGAT	1083
GAGAGTTCAA GGCCAGCCTG GGCCCTGTCA GGACGCTGTC TCAAACAACA GTTTGTTATC	1143
AATAGAATAA TTAGAATTAA CAAACTAGGA TTTTCAGTCT TAAGTCATGA TATTGGATCT	1203
TCCTTTCAGT AAGGTTTCTT TTTGGCTAGA AATACTTCAT AGAATTTGAC ATTTTGGTAT	1263
ACATCTGTGG CCTTGATACA ATGACTTGAT TTTCTGTTTT AATTAGTGCA GAGGATTCAG	1323
CAAATTGCA GGTCTTCATT TTGTTCCCTC GCTATCCATC GATCATGTTT CAGTGTATTA	1383
AGAGGAGTCA GCCAGGCGTG GTGGCCCCACA CCTGTGATCC CAGCACTTAG GGGGGCATAG	1443
GCAGGCAGAT CTCTGTGAGC TGAAGGACAG CCTGGCCTAC AAAGTCCAGG ACAACCGAGA	1503
CCACACAGAG AAACCTTGTC TTGAAAAACA AAACAATAAC AAGAGAGAGA GAGAGAGAGA	1563

Fig. 22G

GAGAAAAGAG	ATGTCAAGAG	GTTTTTGTTT	TTTTTTTTTT	AAATTACTAT	TTATGGGCCT	1623
CAC TTGGAAA	AGTGCTTGCC	ATGCAAAATAG	AAGGACAGGA	GTTCAATCCT	CATTACCCAC	1683
ATTTGAAACA	AATAACAAGA	AAAACAACC	AAAAAACCAA	AACAACAAA	ATCTTGAGAA	1743
CTTGAGTGAA	TACCGGTAAC	CTCAGGGCTA	GGCACTGTAA	CTGAATCAGG	AGCCTCCAGA	1803
TCCAGGGAAA	CGCTGTCTCA	ACAAATAAAT	AAATAAGTAA	GTCAGTGAGG	TGGTCTTTAA	1863
ACCCAGCACT	TGAGAGCCAA	AGCAGGCAG	AGCTCAGTGA	GTTGGAGACC	AGCCTGGTCT	1923
ACAAAGCAAG	TTCTAAGGGA	GCCAGGGCAC	AGAGAAACCC	TGTCGTGAAGG	AAAAAATAAA	1983
AAAAAAAAG	GGCGGCCGC					2002

Fig. 22H

G	1	ATGTTTCTGCTTCTGGTGTTACTCAGCCAGCTGCCCAGACTTACCCTCGC	50
H	1	ATGTTTACGCTTCTGGTTCCTACTCAGCCAACTGCCCCACAGTTACCCCTGGG	50
G	51	GGTTCCCTCAT...ACAAGAAAGCCCTAAAGAAATCTGAAACATGCCCCAGAAAG	97
H	51	GTTTCCCTCATTGCGCAAGAGGTCCAAAGGCTTCTAAGCATGCGGGAGAAG	100
G	98	GAGTCTTTGCATCAAAAAAGCAGCAAGCATCTTTATGCACCGTCGCCCTC	147
H	101	AAGTGTTTACATCAAAAGAAAGCAAACTTTTTCATACATAGACGCCTT	150
G	148	CTATACAATAGATTGTGATTAGAACTCTTCACTCCCGGAACCTGGAGAG	197
H	151	CTGTATAATAGATTGTGATCTGGAGCTCTTCACTCCCGCAACCTAGAAAG	200
G	198	AGAGTGCTATGAGGAGTTCGTAGTTATGAAGAACCCAGAGAGATCCTCG	247
H	201	AGAGTGCAATGAAGAACCTTTCGAATTATGAGGAAGCCAGAGAGATTTTGTG	250

Fig. 22I

G	498	CAGAACCCATGAGGAAGCTGTCTTGTCTCCAT...CGTCAATCCTCAGAGG	544
H	498	CAGAAAGACCTGAGGAGGCTGCCTTGTCTCCATTGCCGCCCTTCTGTGGAGG	547
G	545	ACGCGGGACTACCTTCCCTATGAACAGGCAGTAGCTCTGACCAGAAAAACAC	594
H	548	ATGCAGGATTACCTTCTTATGAACAGGCAGTGGCGCTGACCAGAAAAACAC	597
G	595	AGTGTCTCACCCACCCTCCATATCCTGGGCCAGCAAAAGGATTTAGGGT	644
H	598	AGTGTTTCACCCACCACCACCATATCCTGGGCACACAAAGGATTTAGGGT	647
G	645	ATTTAAAAAGTCAATGTCACTCCCATCTCAC	675
H	648	ATTTAAAAAATCTATGTCTCTCCCATCTCAC	678

Fig. 22K

G	1	M	F	L	L	V	L	S	Q	L	P	R	L	T	L	A	V	P	H	.	T	R	S	L	K	N	S	E	H	A	P	E	G	V	F	A	S	K	K	A	A	S	I	F	M	H	R	R	L	49				
H	1	M	F	T	L	L	V	L	S	Q	L	P	T	V	T	L	G	F	P	H	C	A	R	G	P	K	A	S	K	H	A	G	E	E	V	F	T	S	K	E	E	A	N	F	F	I	H	R	R	L	50			
			
G	50	L	N	R	F	D	L	E	L	F	T	P	G	N	L	E	R	E	C	Y	E	E	F	C	S	Y	E	E	A	R	E	I	L	G	D	N	E	E	M	I	T	F	W	R	E	Y	S	V	K	G	99			
H	51	L	N	R	F	D	L	E	L	F	T	P	G	N	L	E	R	E	C	N	E	E	L	C	N	Y	E	E	A	R	E	I	F	V	D	E	D	K	T	I	A	F	W	Q	E	Y	S	A	K	G	100			
	
G	100	P	T	R	S	D	V	N	K	E	K	I	D	V	M	G	L	L	T	G	L	I	A	A	G	V	F	L	V	V	F	G	L	L	G	Y	L	C	I	T	K	C	N	R	Q	P	Y	Q	G	149				
H	101	P	T	K	S	D	G	N	R	E	K	I	D	V	M	G	L	L	T	G	L	I	A	A	G	V	F	L	V	I	F	G	L	L	G	Y	L	C	I	T	K	C	N	R	L	Q	H	P	C	150				
		
G	150	S	S	A	V	Y	T	R	R	H	T	P	S	I	I	F	R	T	H	E	E	A	V	L	S	P	.	S	S	S	E	D	A	G	L	P	S	Y	E	Q	A	V	A	L	T	R	K	H	198					
H	151	S	S	A	V	Y	.	E	R	G	R	H	T	P	S	I	I	F	R	R	P	E	E	A	L	S	P	L	P	P	S	V	E	D	A	G	L	P	S	Y	E	Q	A	V	A	L	T	R	K	H	199			
			
G	199	S	V	S	P	P	P	P	P	P	G	P	A	K	G	F	R	V	F	K	K	S	M	S	L	P	S	H	225																									
H	200	S	V	S	P	P	P	P	P	P	G	H	T	K	G	F	R	V	F	K	K	S	M	S	L	P	S	H	226																									

Fig. 22L

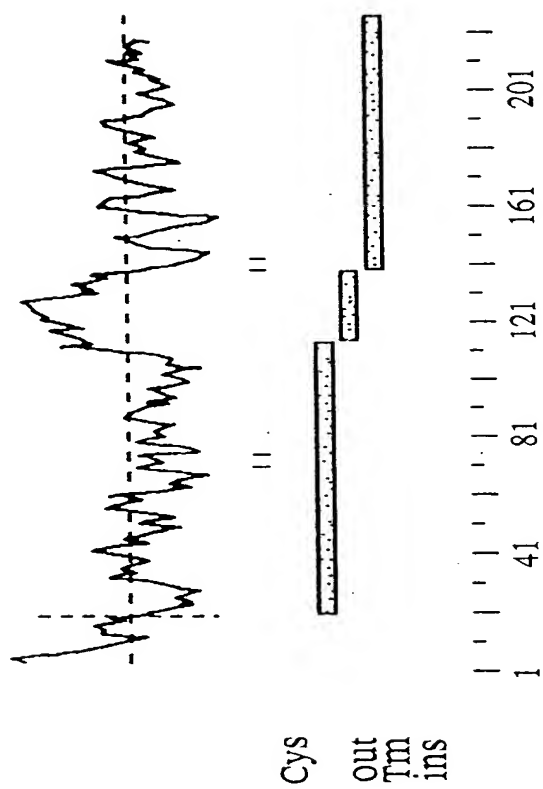


Fig. 22M

T	Y	G	P	D	C	L	A	C	Q	G	G	S	Q	R	P	C	S	G	N	151
ACC	TAC	GGT	CCC	GAC	TGT	CTC	GCA	TGC	CAG	GGC	GGA	TCC	CAG	AGG	CCC	TGC	AGC	GGG	AAT	566
G	H	C	S	G	D	G	S	R	Q	G	D	G	S	C	R	C	H	M	G	171
GGC	CAC	TGC	AGC	GGA	GAT	GGG	AGC	AGA	CAG	GGC	GAC	GGG	TCC	TGC	CGG	TGC	CAC	ATG	GGG	626
Y	Q	G	P	L	C	T	D	C	M	D	G	Y	F	S	S	L	R	N	E	191
TAC	CAG	GGC	CCG	CTG	TGC	ACT	GAC	TGC	ATG	GAC	GGC	TAC	TTC	AGC	TCG	CTC	CGG	AAC	GAG	686
T	H	S	I	C	T	A	C	D	E	S	C	K	T	C	S	G	L	T	N	211
ACC	CAC	AGC	ATC	TGC	ACA	GCC	TGT	GAC	GAG	TCC	TGC	AAG	ACG	TGC	TCG	GGC	CTG	ACC	AAC	746
R	D	C	G	E	C	E	V	G	W	V	L	D	E	G	A	C	V	D	V	231
AGA	GAC	TGC	GGC	GAG	TGT	GAA	GTG	GGC	TGG	GTG	CTG	GAC	GAG	GGC	GCC	TGT	GTG	GAT	GTG	806
D	E	C	A	A	E	P	P	P	C	S	A	A	Q	F	C	K	N	A	N	251
GAC	GAG	TGT	GCG	GCC	GAG	CCG	CCT	CCC	TGC	AGC	GCT	GCG	CAG	TTC	TGT	AAG	AAC	GCC	AAC	866
G	S	Y	T	C	E	E	C	D	S	S	C	V	G	C	T	G	E	G	P	271
GGC	TCC	TAC	ACG	TGC	GAA	GAG	TGT	GAC	TCC	AGC	TGT	GTG	GGC	TGC	ACA	GGG	GAA	GGC	CCA	926
G	N	C	K	E	C	I	S	G	Y	A	R	E	H	G	Q	C	A	D	V	291
GGA	AAC	TGT	AAA	GAG	TGT	ATC	TCT	GGC	TAC	GCG	AGG	GAG	CAC	GGA	CAG	TGT	GCA	GAT	GTG	986

Fig. 23B

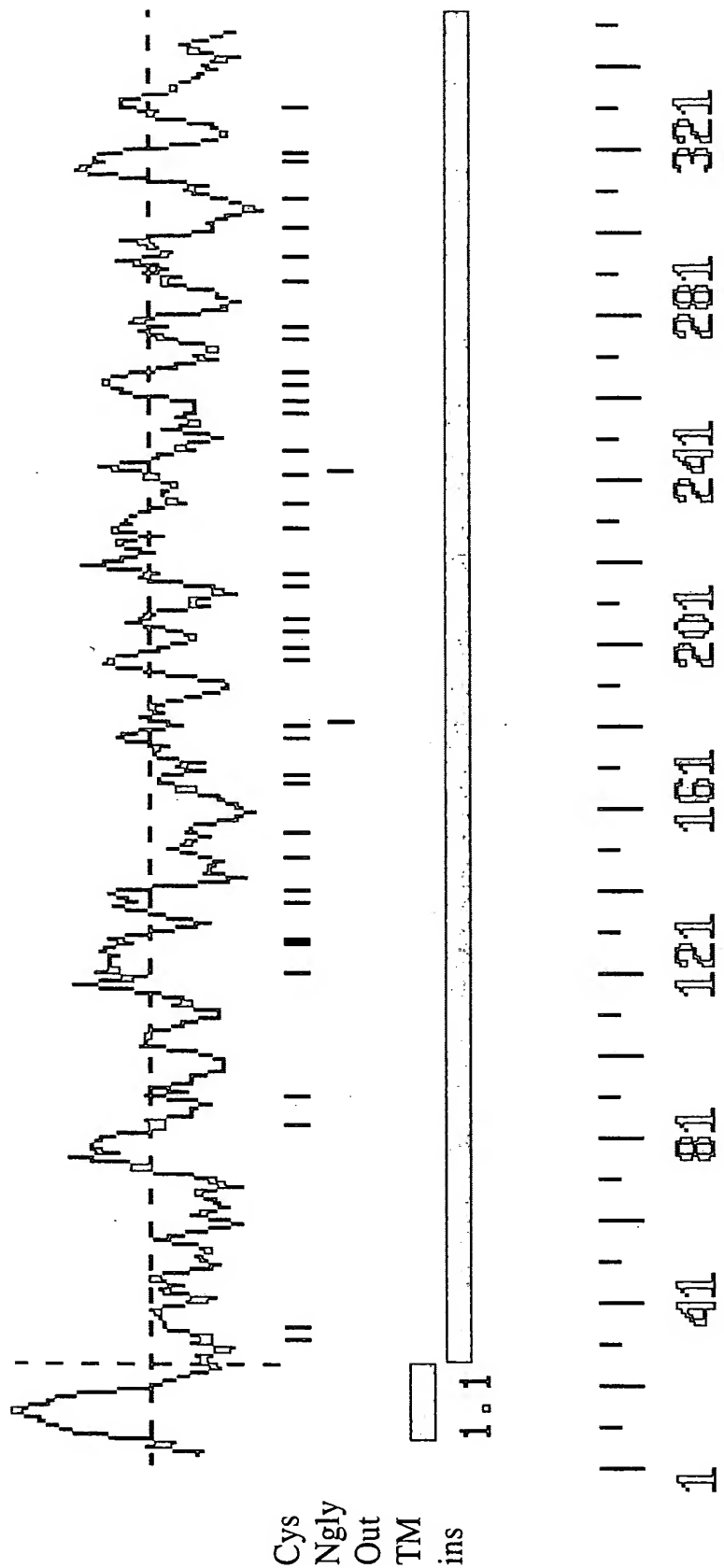


Fig. 23D


```

10      20      30      40      50
C  --GTAGCCGGG--GGAACGGC-CGGC-----GCGCTTG-----CCGGTGGCGGAGGCGAGACT-CCACA
: . : : . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H  ACGCGTCCGCACANGGCCGGCGCGGCTGGGAGCGGGTGGGCGGCCGGAGCGCGGAGCCGGAGCAGCAGCAGCGCCGCA
10      20      30      40      50      60      70

60      70      80      90      100      110
C  G---CAGTT-CTC-TGCCG-GTCG-CCCGCGAGTGC-ACCCGCCATGCACCTGCCGC-CCGCTGCCGCAG
: . : : . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H  GGACCTGGAGCTCCGGCTGCGTCTTCCCGC-AGCGCTACCCGCCATGCGCCTGCCGCGCGC-GGCCGCGC
80      90      100      110      120      130

120      130      140      150      160      170      180
C  TCGGGCT---GCTACTGCTGCTGCTGCCGCTCCCGCGCGTGCGCTCCCGGAAGCCGACAATGTGCCA
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H  TGGGGCTCCTGCCGCTTCTGCTGCTGCTGCCGCCCGCGCGGAGCGCCCAAGAAGCCGACGCCCTGCCA
140      150      160      170      180      190      200

190      200      210      220      230      240      250
C  GAGGTGCCGGGGCGCTGGTGGACAAGTTCAACCAGGGGATGGCCACACAGGCCAGGAAGAAATTCGGCGGC
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H  CCGGTGCCGGGGCGCTGGTGGACAAGTTTAACCAGGGGATGGTGGACACCCGCAAGAAGAACTTTGGCGGC
210      220      230      240      250      260      270

```

Fig. 23F

```

260      270      280      290      300      310      320
C GGCAACACGGCGTGGGAGGAGAAGAGTCTGTCCAAGTACGAATTCAGTGAGATTGGCTCCTGGAGATTA
  :: :::::::::: :::::::::: :::::::::: :::::::::: :::::::::: ::::::::::
280      290      300      310      320      330      340
H GGGAACACGGCTTGGGAGGAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTCCGCTGCTGGAGATCC

330      340      350      360      370      380      390
C TGGAGGGCCTGTGTGACAGCAACGACTTTGAATGCAACCAACT-CTTGGAAACAGCATGAGGAGCAGCTAG
  :::::::::: :::::::::: :::::::::: :::::::::: :::::::::: ::::::::::
350      360      370      380      390      400      410
H TGGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGC-GCAGGAGGAGCACCTGG

400      410      420      430      440      450      460
C AGGCCCTGGTGGCAGACACTGAAGAAGGAGTGCCCTAACCTATTGAGTGGTTCTGTGTACACACTGAA
  :::::::::: :::::::::: :::::::::: :::::::::: :::::::::: ::::::::::
420      430      440      450      460      470      480
H AGGCCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTTTGTGTGAAGACACTGAA

470      480      490      500      510      520      530
C AGCATGCTGTCTTCCAGGCACCTATGGGCCAGACTGTTCAGGAATGCCAGGTTGGTCTCAGAGGCCCTTGT
  :::::::::: :::::::::: :::::::::: :::::::::: :::::::::: ::::::::::
490      500      510      520      530      540      550
H AGTGTGCTGTCTCCAGGAACCTACGGTCCCAGCTGTCTCGCATGCCAGGGCGGATCCCAGAGGCCCTGC

```

Fig. 23G


```

540      550      560      570      580      590      600
C  AGCGGGAATGGCCACTGCGACGGAGATGGCAGCAGACAGGCGACGGGTCTCTGCCAGTGTCACTAGGAT
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
H  AGCGGGAATGGCCACTGCGACGGAGATGGGAGCAGACAGGCGACGGGTCTCTGCCGTGCCACATGGGGT
560      570      580      590      600      610      620

610      620      630      640      650      660      670
C  ACAAGGGCCCGCTGTGTATCGACTGCATGGATGGCTACTTCAGCTTGCTGAGGAACGAGACCCACAGCTT
   ::::::::::: : :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
H  ACCAGGGCCCGCTGTGCACTGCACTGACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCAT
630      640      650      660      670      680      690

680      690      700      710      720      730      740
C  CTGCACAGCCCTGTGATGAGTCCCTGCAAGACATGCTCAGGTCCAACCAACAAGGCTGTGTGGAGTCCGAA
   :::::::::::::: :::::::::::::: :::::::::::::: : :::::::::::::: : ::::::::::::::
H  CTGCACAGCCCTGTGACGAGTCCCTGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAA
700      710      720      730      740      750      760

750      760      770      780      790      800      810
C  GTGGGCTGGACACGTGTGGAGGATGCCCTGTGTGGATGTTGACGAGTGTGCAGCAGAGACCCACCCCTGCA
   ::::::::::. . : ::::: :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
H  GTGGGCTGGGTGCTGGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGGCCGAGCCGCCCTCCCTGCA
770      780      790      800      810      820      830

```

Fig. 23H

```

      820      830      840      850      860      870      880
C  GCAATGTACAGTACTGTGAAAATGTCAACGGCTCCTACACATGTGAAGAGTGTGATTCTACCTGTGTGGG
   :: :: :::::::::::::: :: :::::::::::::: :: :::::::::::::: :: ::::::::::::::
H  GCGCTGCCGAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTGTGGG
840      850      860      870      880      890      900

      890      900      910      920      930      940      950
C  CTGCACAGGAAAAGGCCCCAGCCAATTGTAAAGAGTGTATCTCTGGCTACAGCAAGCAGAAAGGAGAGTGT
   :::::::::::::: :: :::::::::::::: :::::::::::::: :: :: :: :: :: :: :: :: :: :: :: :: ::
H  CTGCACAGGGGAAGGCCCCAGGAAACTGTAAAGAGTGTATCTCTGGCTACGCGAGGGAGCAGCACGACAGTGT
910      920      930      940      950      960      970

      960      970      980      990      1000      1010      1020
C  GCAGATATAGATGAATGCTCATTAGAAAACAAAGGTGTGTAAGAAAGGAAAAATGAGAACTGCTACAATACTC
   :::::::::::::: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
H  GCAGATGTGGACGAGTGTCTACTAGCAGAAAAAACCTGTGTGAGGAAAAAACGAAAACTGCTACAATACTC
980      990      1000      1010      1020      1030      1040

      1030      1040      1050      1060      1070      1080      1090
C  CAGGGAGCTTTTGTCTGCGTGTGTCCGGAAGGTTTCGAGGAAGACAGAAAGATGCTTGTGTACAGACAGCAG
   :::::::::::::: :: :: :::::::::::::: :: :::::::::::::: :::::::::::::: :: :: :: :: :: :: :: :: :: ::
H  CAGGGAGCTACGTCTGTGTGTCTGACGGCTTCGAAGAA-ACGGAAGATGCCCTGTGTGTCGCCCGCCGCGCAG
1050      1060      1070      1080      1090      1100      1110

```

Fig. 23I

```

1100      1110      1120      1130      1140      1150
C AAGCGAAGTGGCAGAGGAAAGT--CCC-ACACAGCCACCCTCCCATGAGGATTGTGACGGGCATCCAG
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H AGGCTGAAGCCACAGAAGGAGAAAGCCCGACACAGCTGCCCTCCCGCGAAGA-----CCTG
1120      1130      1140      1150      1160      1170
1160      1170      1180      1190      1200      1210      1220
C GTTCAGAAAGCTGGACTCTCACCCCTTTTAAGTTATTGAGAGGACATCCTATAGAAAAATGTGCCCCATGGAC
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H --TAATGTGCCGGGACTT--ACCCTTTAAATTATTCAGAAAGGATGTCCCCTGGAAAAATGTGGCCCTGAGGA
1180      1190      1200      1210      1220      1230

1230      1240      1250      1260      1270      1280      1290
C ATCAACCCCATTTCTCCAGGAAGTTTGG-AGGAAGAAGCTGCCTGCTTTGAAACAGTAGATACTCACTT
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H TGCCGTCTC---CTGCAGTGGACAGCGGGGGGAGAGGCTGCCTGCTCTCTAAACGGTTGATTCTCATTT
1240      1250      1260      1270      1280      1290      1300
1300      1310      1320      1330      1340      1350      1360
C GGCCCTTTAAAACGCTGCATTTCTTGGTGGTTCTTAAACAGATTTCGTATATTTTGATACTGTTCTTTATA
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H GTCCCTTAAACA-GCTGCATTTCTTGGTGTGTTCTTAAACAGACTTGTATATTTTGATACAGTTCCTTGTGA
1310      1320      1330      1340      1350      1360      1370

1370      1380      1390
C ATAAAATTGATCATTTGAAGGTCACCAGGAA-----CA-----
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H ATAAAATTGACCATTGTAGGTAATCAAAAAAAAAAAAAAAAAAGGCGCGCGCTAGAC
1380      1390      1400      1410      1420      1430

```

Fig. 23J

GTCGACCCACGGTCCGTCCCTGCGGGCCCCAGCCCTCTCCTCACGCTCGCGCAGTCTCCGCCGCAGTCTCAGCTGCAGCTG	79
CAGGACTGAGCCCGTGACCCCGGAGGAGACCCCGGAGGAGCGACAAACTTCGCAGTGCCCGCGACCCCAACCCAGCCCT	158
<div style="display: flex; justify-content: space-between;"> <div> M A Q L F L P L L A A L V L A Q </div> <div> GGTAGCCTGCAGC ATG GCC CAG CTG TTC CTG CCC CTG CTG GCA GCC CTG GTC CTG GCC CAG </div> </div>	<div style="display: flex; justify-content: space-between;"> <div>16</div> <div>220</div> </div>
<div style="display: flex; justify-content: space-between;"> <div> A P A A L A D V L E G D S S E D R A F R </div> <div> GCT CCT GCA GCT TTA GCA GAT GTT CTG GAA GGA GAC AGC TCA GAG GAC CGC GCT TTT CGC </div> </div>	<div style="display: flex; justify-content: space-between;"> <div>36</div> <div>280</div> </div>
<div style="display: flex; justify-content: space-between;"> <div> V R I A G D A P L Q G V L G G A L T I P </div> <div> GTG CGC ATC GCG GGC GAC GCG CCA CTG CAG GGC GTG CTC GGC GCC CTC ACC ATC CCT </div> </div>	<div style="display: flex; justify-content: space-between;"> <div>56</div> <div>340</div> </div>
<div style="display: flex; justify-content: space-between;"> <div> C H V H Y L R P P P S R R A V L G S P R </div> <div> TGC CAC GTC CAC TAC CTG CGG CCA CCG AGC CGC GCT GTG CTG GGC TCT CCG CGG </div> </div>	<div style="display: flex; justify-content: space-between;"> <div>76</div> <div>400</div> </div>
<div style="display: flex; justify-content: space-between;"> <div> V K W T F L S R G R E A V L V A R G V </div> <div> GTC AAG TGG ACT TTC CTG TCC CGG GGC CGG GAG GCA GAG GTG CTG GCG GGA GTG </div> </div>	<div style="display: flex; justify-content: space-between;"> <div>96</div> <div>460</div> </div>
<div style="display: flex; justify-content: space-between;"> <div> R V K V N E A Y R F R V A L P A Y P A S </div> <div> CGC GTC AAG GTG AAC GAG GCC TAC CGG TTC CGC GTG GCA CTG CCT GCG TAC CCA GCG TCG </div> </div>	<div style="display: flex; justify-content: space-between;"> <div>116</div> <div>520</div> </div>
<div style="display: flex; justify-content: space-between;"> <div> L T D V S L A L S E L R P N D S G I Y R </div> <div> CTC ACC GAC GTC TCC CTG GCG CTG AGC GAG CTG CGC CCC AAC GAC TCA GGT ATC TAT CGC </div> </div>	<div style="display: flex; justify-content: space-between;"> <div>136</div> <div>580</div> </div>

Fig. 24A

C	E	V	Q	H	G	I	D	D	S	S	A	V	E	V	K	V	K	G	156	
TGT	GAG	GTC	CAG	CAC	GAC	ATC	GAT	GAC	AGC	AGC	GAC	GCT	GTG	GAG	GTC	AAG	GTC	AAA	GGG	640
V	V	F	L	Y	R	E	G	S	A	R	Y	A	F	S	F	S	G	A	Q	176
GTC	GTC	TTT	CTC	TAC	CGA	GAG	GGC	TCT	GCC	CGC	TAT	GCT	TTC	TCC	TTT	TCT	GGG	GCC	CAG	700
E	A	C	A	R	I	G	A	H	I	A	T	P	E	Q	L	Y	A	A	Y	196
GAG	GCC	TGT	GCC	CGC	ATT	GGA	GCC	CAC	ATC	GCC	ACC	CCG	GAG	CAG	CTC	TAT	GCC	GCC	TAC	760
L	G	G	Y	E	Q	C	D	A	G	W	L	S	D	Q	T	V	R	Y	P	216
CTT	GGG	GGC	TAT	GAG	CAA	TGT	GAT	GCT	GGC	TGG	CTG	TCG	GAT	CAG	ACC	GTG	AGG	TAT	CCC	820
I	Q	T	P	R	E	A	C	Y	G	D	M	D	G	F	P	G	V	R	N	236
ATC	CAG	ACC	CCA	CGA	GAG	GCC	TGT	TAC	GGA	GAC	ATG	GAT	GGC	TTC	CCC	GGG	GTC	CGG	AAC	880
Y	G	V	V	D	P	D	D	L	Y	D	V	Y	C	Y	A	E	D	L	N	256
TAT	GGT	GTG	GTG	GAC	CCG	GAT	GAC	CTC	TAT	GAT	GTG	TAC	TGT	TAT	GCT	GAA	GAC	CTA	AAT	940
G	E	L	F	L	G	D	P	P	E	K	L	T	L	E	E	A	R	A	Y	276
GGA	GAA	CTG	TTC	CTG	GGT	GAC	CCT	CCA	GAG	AAG	CTG	ACA	TTG	GAG	GAA	GCA	CGG	GCG	TAC	1000
C	Q	E	R	G	A	E	I	A	T	T	G	Q	L	Y	A	A	W	D	G	296
TGC	CAG	GAG	CGG	GGT	GCA	GAG	ATT	GCC	ACC	ACG	GGC	CAA	CTG	TAT	GCA	GCC	TGG	GAT	GGT	1060

Fig. 24B

G	L	D	H	C	S	P	G	W	L	A	D	G	S	V	R	Y	P	I	V	316
GGC	CTG	GAC	CAC	TGC	AGC	CCA	GGG	TGG	CTA	GCT	GAT	GGC	AGT	GTG	CGC	TAC	CCC	ATC	GTC	1120
T	P	S	Q	R	C	G	G	G	L	P	G	V	K	T	L	F	L	F	P	336
ACA	CCC	AGC	CAG	CGC	TGT	GGT	GGG	GGC	TTG	CCT	GGT	GTC	AAG	ACT	CTC	TTC	CTC	TTC	CCC	1180
N	Q	T	G	F	P	N	K	H	S	R	F	N	V	Y	C	F	R	D	S	356
AAC	CAG	ACT	GGC	TTC	CCC	AAT	AAG	CAC	AGC	CGC	TTC	AAC	GTC	TAC	TGC	TTC	CGA	GAC	TCG	1240
A	Q	P	S	A	I	P	E	A	S	N	P	A	S	N	P	A	S	D	G	376
GCC	CAG	CCT	TCT	GCC	ATC	CCT	GAG	GCC	TCC	AAC	CCA	GCC	TCC	AAC	CCA	GCC	TCT	GAT	GGA	1300
L	E	A	I	V	T	V	T	E	T	L	E	E	L	Q	L	P	Q	E	A	396
CTA	GAG	GCT	ATC	GTC	ACA	GTG	ACA	GAG	ACC	CTG	GAG	GAA	CTG	CAG	CTG	CCT	CAG	GAA	GCC	1360
T	E	S	E	S	R	G	A	I	Y	S	I	P	I	M	E	D	G	G	G	416
ACA	GAG	AGT	GAA	TCC	CGT	GGG	GCC	ATC	TAC	TCC	ATC	CCC	ATC	ATG	GAG	GAC	GGA	GGA	GGT	1420
G	S	S	T	P	E	D	P	A	E	A	P	R	T	L	L	E	F	E	T	436
GGA	AGC	TCC	ACT	CCA	GAA	GAC	CCA	GCA	GAG	GCC	CCT	AGG	ACG	CTC	CTA	GAA	TTT	GAA	ACA	1480
Q	S	M	V	P	P	T	G	F	S	E	E	E	G	K	A	L	E	E	E	456
CAA	TCC	ATG	GTA	CCG	CCC	ACG	GGG	TTC	TCA	GAA	GAG	GAA	GGT	AAG	GCA	TTG	GAG	GAA	GAA	1540

Fig. 24C

E	K	Y	E	D	E	E	E	E	E	E	E	E	V	E	D	476	
GAG	AAA	TAT	GAA	GAT	GAA	GAG	AAA	GAG	GAA	GAA	GAG	GAG	GTG	GAG	GAT	1600	
E	A	L	W	A	W	P	S	E	L	S	S	P	G	P	E	A	496
GAG	GCT	CTG	TGG	GCA	TGG	CCC	AGC	GAG	CTC	AGC	AGC	CCG	GGC	CCT	GAG	GCC	1660
T	E	P	A	A	Q	E	K	S	L	S	Q	A	P	A	R	A	516
ACT	GAG	CCA	GCA	GCC	CAG	CAG	AAG	TCA	CTC	TCC	CAG	GCG	CCA	GCA	AGG	GCA	1720
P	G	A	S	P	L	P	D	G	E	S	E	A	S	R	P	P	536
CCT	GGT	GCA	TCA	CCA	CTT	CCT	GAT	GGA	GAG	TCA	GAA	GCT	TCC	AGG	CCT	CCA	1780
G	P	P	T	E	T	L	P	T	P	R	E	R	N	L	A	S	556
GGA	CCA	CCT	ACT	GAG	ACT	CTG	CCC	ACT	CCC	AGG	GAG	AGG	AAC	CTA	GCA	TCC	1840
S	T	L	V	E	A	R	E	V	G	E	A	T	G	G	P	E	576
TCC	ACT	CTG	GTT	GAG	GCA	AGA	GAG	GTG	GGG	GAG	GCA	ACT	GGT	GGT	CCT	GAG	1900
V	P	R	G	E	S	E	E	T	G	S	S	E	G	A	P	S	596
GTC	CCT	CGA	GGA	GAG	AGC	GAG	GAG	ACA	GGA	AGC	TCC	GAG	GGT	GCC	CCT	TCC	1960
A	T	R	A	P	E	G	T	R	E	L	E	A	P	S	E	D	616
GCC	ACA	CGG	GCC	CCT	GAG	GGT	ACC	AGG	GAG	CTG	GAG	GCC	CCC	TCT	GAA	GAT	2020

Fig. 24D

R	T	A	P	A	G	T	S	V	Q	A	Q	P	V	L	P	T	D	S	A		636
AGA	ACT	GCC	CCA	GCA	GGG	ACC	TCA	GTG	CAG	GCC	CAG	CCA	GTG	CTG	CCC	ACT	GAC	AGC	GCC		2080
S	R	G	G	V	A	V	V	P	A	S	G	N	S	A	Q	G	S	T	A		656
AGC	CGA	GGT	GGA	GTG	GCC	GTG	GTC	CCC	GCA	TCA	GGT	AAT	TCT	GCC	CAA	GGC	TCA	ACT	GCC		2140
L	S	I	L	L	L	F	F	P	L	Q	L	W	V	T	*						672
CTC	TCT	ATC	CTA	CTC	CTT	TTC	TTC	CCC	CTG	CAG	CTC	TGG	GTC	ACC	TGA						2188
CCT	GTAG	TCCTT	TAA	CCCC	ACCAT	CAT	CCCC	AACT	CTC	CTGT	CTCTT	TGCC	TTCA	TTCT	TAC	CCAC	CTCT	ACCT	ATGGG		2267
TCT	CCAA	TCT	CGG	ATAT	CCAC	CTT	GTG	GGT	ATCT	CAG	CTCT	CCG	CGT	CTTT	ACC	CTGT	GAT	CC	CAG	CCCC	2346
CAT	CTGT	GAC	CCCT	TCCC	AT	TGG	GGCC	CTCC	ACCT	GTGG	CTC	ACAT	CTCG	CCAG	CCCC	ACAG	AGCAT	CTC	AGGC	CT	2425
CT	CCAA	GGGT	CTCAT	CAC	CTAT	TGC	AG	CCCT	T	CAG	GGCT	CGG	CTAT	TTT	CCAC	TACT	CCCT	TCAT	CCGC	CTGT	2504
GT	CCCC	TTAG	CTGC	CTC	AT	TGAT	CTC	AGG	GAAG	CCCT	TGG	AGT	CCCT	TTCT	CAC	CCCT	CAAC	CTCC	GGAG	TCC	2583
AA	CCCG	TAC	CCCC	ACAG	AG	CCCTT	AA	GCA	ACT	ACT	TTCT	GTG	AAG	TAT	TTTT	TGAC	TGTT	TCAT	GGAAA	CAAG	2662
AA	TAA	ATCT	CTAT	TAA	ACCG	CTTT	TG	TAA	CCAAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	GGG	2730

Fig. 24E

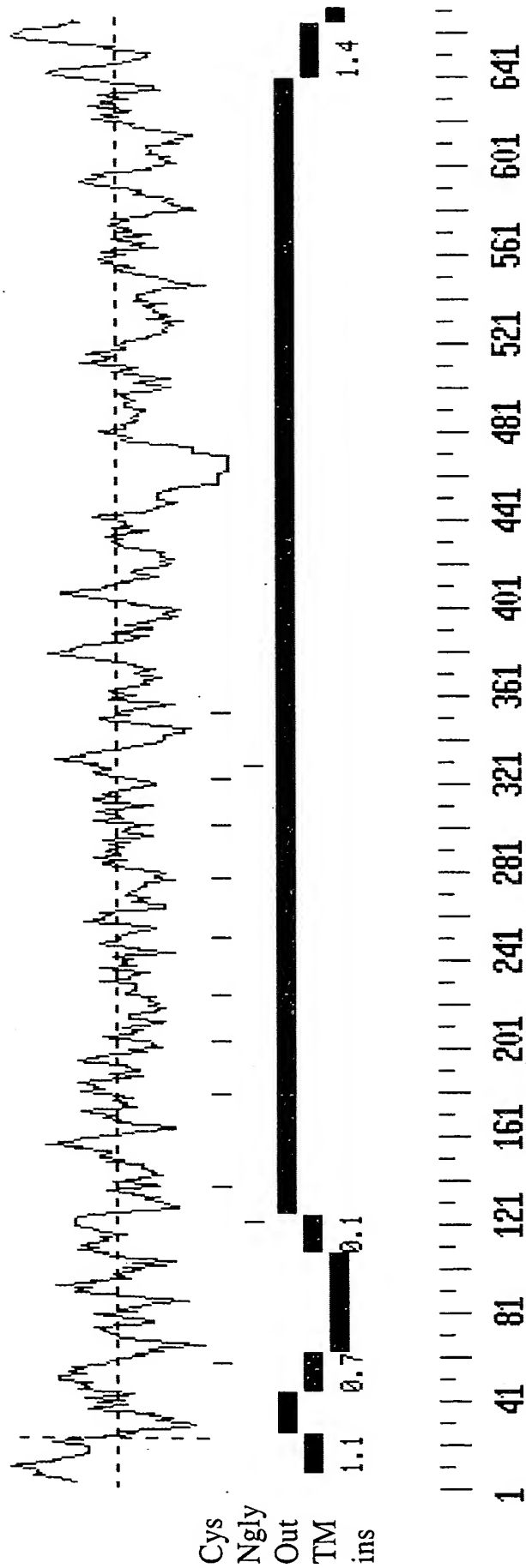


Fig. 24F

332	MAQFLPLLAALVLAQAPAAALADVLEGDSS	EDRAFRVRIAGDAPLQGVLGALTIPCHVHVYLRPPPSRRA	10	20	30	40	50	60	70
BEF	MAQFLPLLAALVLAQAPAAALADVLEGDSS	EDRAFRVRIAGDAPLQGVLGALTIPCHVHVYLRPPPSRRA	10	20	30	40	50	60	70
332	VLGSPRVKWTFLSRGREA	EVLVARGVVRVKVNEAYRFRVALPAYPASLTDVSLALSELRPNDSGIYRCEVQ	80	90	100	110	120	130	140
BEF	VLGSPRVKWTFLSRGREA	EVLVARGVVRVKVNEAYRFRVALPAYPASLTDVSLALSELRPNDSGIYRCEVQ	80	90	100	110	120	130	140
332	HGIDDS	DAVEVKVG	VFLYREGSARYAFSFGAQ	EACARIGAHIA	TP	EQLYAA	YLGGEQCDAGW	LSD	
BEF	HGIDDS	DAVE							
332	QTVRYPIQTPREACYGDM	DFPGVRNYGVVDPDDL	YDVYCYAED	NLGELFLGDPPEKLTLEE	ARAYCQER				
BEF	QTVRYPIQTPREACYGDM	DFPGVRNYGVVDPDDL	YDVYCYAED	NLGELFLGDPPEKLTLEE	ARAYCQER				
332	GAEIATTGQLYAAWDGGLD	HCSPGWLADG	SVRYPIVTPSQRCGGGLPGVKTLFLFP	NOTGFPNKH	SRFNV				
BEF	GAEIATTGQLYAAWDGGLD	HCSPGWLADG	SVRYPIVTPSQRCGGGLPGVKTLFLFP	NOTGFPNKH	SRFNV				

Fig. 24G

```

360      370      380      390      400      410
332 YCFRDSAQP-SAIPEASNPA SDGLEAIVTVTETLEELQLPQEATESESRGAIYSIPIMEDGGGGSS
      :::::  ...  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
BEF YCFRDSAQLPSLRPPTQPPTQL--DGLEAIVTVTETLEELQLPQEATESESRGAIYSIPIMEDGGGGSS
      300      310      320      330      340      350

420      430      440      450      460      470      480
332 TPEDPAEAPRTLLEFFETQSMVPPPTGFSEEEGKALEEEKYEDEEEKEEEEEVEDEALWAWPSELSSP
      :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
BEF TPEDPAEAPRTLLEFFETQSMVPPPTGFSEEEGKALEEEKYEDEEEKEEEEEVEDEALWAWPSELSSP
360      370      380      390      400      410      420

490      500      510      520      530      540      550
332 GPEASLPTEPAAQEKSLSQAPARAVLQPGASPLPDGESEASRPPRVHGPPTETLTPPRENLASPSSTL
      :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
BEF GPEASLPTEPAAQEESSLSQAPARAVLQPGASPLPDGESEASRPPRVHGPPTETLTPPRENLASPSSTL
430      440      450      460      470      480      490

560      570      580      590      600      610      620
332 VEAREVGEATGGPELSGVPRGESEETGSSEGAPSLPATRAPEGTRELEAPSEDNSGR TAPAGTSVQAQP
      :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
BEF VEAREVGEATGGPELSGVPRG-----GAR-----TQ-
500      510      520

630      640      650      660      670
332 VLPTDSASRGGVAVVPASGNSAQQSTALSILLFFFLQLWVT
      :::::  :::::  :::::  :::::  :::::
BEF -----FAL-----

```

Fig. 24H

10	20	30	40	50	60
M	MIPLLLSLLAALVLTQAPAAALADDLKEDSSEDRAFRVRI-GAAQLRGVLGGALAI	PC	HV	HL	RP
:	:	:	:	:	:
H	MAQLFLPLLAALVLAQAPAAALADVLEGDSSEDRAFRVRIAGDAPLQGV	LGG	ALT	IP	CH
10	20	30	40	50	60
70	80	90	100	110	120
M	APGFPRVKWTF	LSG	REVEVLVARGLRVKVNEAYRFRVALPAYPASLTDVSLV	SEL	RPNDSGVYRCEVQ
:	:	:	:	:	:
H	VLGS	PRVKWTF	LSR	GREAEVLVARGVRVKVNEAYRFRVALPAYPASLTDVSL	ALSEL
80	90	100	110	120	130
140	150	160	170	180	190
M	HGIDSSDAVEVKVG	VFLYREGSARYAFS	FAGAQA	CARIGARIATPEQLY	AAVLGGYEQCDAGW
:	:	:	:	:	:
H	HGIDSSDAVEVKVG	VFLYREGSARYAFS	FAGAQA	CARIGAHIA	TPEQLY
150	160	170	180	190	200
210	220	230	240	250	260
M	QTVRYP	IQNP	REACSG	MDGYPGVRNYGV	GPDDLDYDV
:	:	:	:	:	:
H	QTVRYP	IQTP	REAC	YGDMDGFP	GVNRNYGVDPDDLDYDV
220	230	240	250	260	270
280	290	300	310	320	330
M	GAQLASTGQ	LYAAWNGGLDR	CSPGWLADG	SVRYP	PIITPSQRCGGGLPGV
:	:	:	:	:	:
H	GAEIAT	TGQ	LYAAWDGGLDH	CSPGWLADG	SVRYP
290	300	310	320	330	340
350	360	370	380	390	400

Fig. 24I

	680	690	700	710	720	730	740
M	GACYKHFS	TRRSWEAE	SQCRA	LGAHLT	SICTPEEQD	FVNDRYREYQ	WIGLNDRTIEGDFLWSDGAPLLY
H	-----SI-----L-----LLF						660
	750	760	770	780	790	800	810
M	ENWNP	GGPDSY	FLSGENC	VVMVWHD	QGWSDV	PCNYHLSY	TCKMGLVSCGPPQLPLAQIFGRPRLRYAV
H	-----F-----PLQ-----						
	820	830	840	850	860	870	880
M	DTVLR	YRCRD	GLAQR	NLPLIRC	QENGLWE	APQISCV	PRRPGRALRSMDAPEGPRGQLSRHRKAPLTPPSS
H	-----LWVT-----						670

M L
H -

Fig. 24K

```

10      20      30      40      50
H  GTCG-ACCCA-CG-----CGTCC-----GTCCCTGGGCCCCAGCCTCTCCTCAGCTCGCGCAGTC
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M  GAGGCTCCCGCGAGCTGGCGCCCCCTGTCTGGGTCCCGCGCGCCCGGCC-CTGCTCGCGCCCGCGCA-TC
   10      20      30      40      50      60

60      70      80      90      100     110     120
H  TCCGCCGCAGTCTCAG-CTGCAGCTGCAGGACTGAGCCGTGCACCCGGAGGAGACCCCGGAGAGGCGGA
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M  GC-GCCGCAGTCTCGGTCTGCGGCTGCGGACGTGACGGCGTGC GCGGAGGGACCTC-----GCAA
   70      80      90      100     110     120

130     140     150     160     170     180     190
H  CAAACTTCGAGTGCCCGGACCCCAACCCAGCCCTGGGTAGCCTGCAGCATGGCCAGCTGTTCTCTGCCC
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M  -GTTCTTC-----CATC-----AGTG---TGCAGAAATGATACCACCTGCTTCTGTCC
   130     140     150     160     170

200     210     220     230     240     250     260
H  CTGCTGGCAGCCCTGGTCCCTGGCCCCAGGCTCCTGCAGCTTTAGCAGATGTTCTGGAAGGAGACAGCTCAG
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M  CTGCTGGCCGCTCTGGTCCCTGACCCCAAGCCCCCTGCCGCCCTCGCTGATGACCTGAAAGAAGACAGCTCGG
   180     190     200     210     220     230     240

270     280     290     300     310     320     330
H  AGGACCGCGCTTTTCGCGTGCGCATCGCGGGCGACGCGCCACTGCAGGGCGTGCTCGGCGGCCCTCAC
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M  AGGATCGAGCCTTCCGCGTGCGCATCG-GTGC--CGCGCAGCTGCGGGGCGTGCTGGGCGGTGCCCTGGC
   250     260     270     280     290     300

```

Fig. 24L

```

340      350      360      370      380      390      400
H CATCCCTTGCCACGTCCACTACCTGCGGCCACCGCCGAGCCGCGGCTGTGCTGGCTCTCCGGGGTC
   :::::::::::::::::::::::::::::::::::::::::::::::::::: : : : : : : : : : : : :
M CATCCCATGCCACGTCCACCACTGCGGCCCGCGCGCAGCCGCGCGCGCGGGTTTTCCTCCCGGGTC
310      320      330      340      350      360      370

410      420      430      440      450      460      470
H AAGTGGACTTTCCTGTCCCGGGCGGAGGCAGAGGTGCTGGTGGCGGGGAGTGCGCGTCAAGGTGA
   :::::::::::::::::::::::::::::::::::::::::::::::::::: : : : : : : : : : : : :
M AAGTGGACCTTCCTGTCCGGGACCGGAGGTAGAGGTTCGTGGCTCGCGGGCTGCGCGTCAAGGTAA
380      390      400      410      420      430      440

480      490      500      510      520      530      540
H ACGAGGCCCTACCGGTTCCGCGTGGCACTGCCCTGCGTACCCAGCGTCGCTACCGACGTCTCCCTGGCGCT
   :::::::::::::::::::::::::::::::::::::::::::::::::::: : : : : : : : : : : : :
M ACGAAGCCTACCGGTTCCGCGTGGCGCTGCCCTACCCCGCATCGCTACGGATGTGTCTCTAGTATT
450      460      470      480      490      500      510

550      560      570      580      590      600      610
H GAGCGAGCTGCGCCCCAACGACTCAGGTATCTATCGCTGTGAGGTCCAGCACGGCATCGATGACAGCAGC
   :::::::::::::::::::::::::::::::::::::::::::::::::::: : : : : : : : : : : : :
M GAGCGAACTGCGGGCCCAATGATTCCGGGGTCTATCGCTGCGAGGTCCAGCACGGTATCGACGACAGCAGT
520      530      540      550      560      570      580

620      630      640      650      660      670      680
H GACGCTGTGGAGGTCAAGGTCAAAGGGTTCGTCTTTCTCTACCGAGAGGGCTCTGCCCGCTATGCTTTCT
   :::::::::::::::::::::::::::::::::::::::::::::::::::: : : : : : : : : : : : :
M GATGCTGTGGAGGTCAAGGTCAAAGGGTTCGTCTTCTCTACAGAGAGGGCTCTGCGCGCTATGCTTTCT
590      600      610      620      630      640      650

```

Fig. 24M


```

690      700      710      720      730      740      750
H CCTTTCTGGGGCCAGGAGGCCTGTGCCCCGCAATTGGAGCCACATCGCCACCCCGGAGCAGCTCTATGC
   :::::::::::::::::::: : :::::::::::::::::::: : :::::::::::::::::::: :
M CCTTCGCTGGAGCCCAAGGAGCCTGCGCTCGCATAGGAGCCCGAATCGCCACCCCGGAGCAGCTCTATGC
660      670      680      690      700      710      720

760      770      780      790      800      810      820
H CGCCTACCTTGGGGCTATGAGCAATGTGATGCTGGCTGGCTGTCGGATCAGACCGTGAGGTATCCCATC
   :::::::::::::::::::: : :::::::::::::::::::: : :::::::::::::::::::: :
M TGCCTACCTCGGCGGCTATGAGCAGTGTGATGCAGGCTGGCTGTCCGACCAAACTGTGAGGTACCCCATC
730      740      750      760      770      780      790

830      840      850      860      870      880      890
H CAGACCCCAAGAGGCCTGTACGGAGACATGGATGGCTTCCCCGGGTCCGAACTATGGTGTGGTGG
   :::::::::::::::::::: : :::::::::::::::::::: : :::::::::::::::::::: :
M CAGAACCCCAAGAGGCCTGTCTGGAGACATGGATGGCTATCCTGGCGTGCAGAACTACGGAGTGGTGG
800      810      820      830      840      850      860

900      910      920      930      940      950      960
H ACCCGGATGACCTCTATGATGTGTACTGTTATGCTGAAGACCTAAATGGAGAACTGTTCTCTGGGTGACCC
   . :::::::::::::::::::: : :::::::::::::::::::: : :::::::::::::::::::: :
M GTCCTGATGATCTCTATGATGTCTACTGTTATGCCGAAGACCTAAATGGAGAACTGTTCTCTAGGCGCCCC
870      880      890      900      910      920      930

970      980      990      1000      1010      1020      1030
H TCCAGAGAAAGCTGACATTGGAGGAAGCACGGGCGTACTGCCAGGAGCGGGGTGCAGAGATTGCCACCACG
   :: . :::::::::::::::::::: : :::::::::::::::::::: : :::::::::::::::::::: :
M TCCCAGCAAAGCTGACATGGGAGGAGGCTCGGGACTACTGTCTGGAACGTGGTGCACAGATCGCTAGCACA
940      950      960      970      980      990      1000

```

Fig. 24N

1040	1050	1060	1070	1080	1090	1100
H	GGCCAACTGTATGCAGCCTGGGATGGTGGCCTGGACCACTGCAGCCAGGGTGGCTAGCTAGTGGCAGTG					
M	GGCCAGCTGTACGCAGCCTGGAATGGTGGCCTGGACAGATGTAGCCCTGGCTGGCTGGCTGATGGCAGCG					
1010	1020	1030	1040	1050	1060	1070
1110	1120	1130	1140	1150	1160	1170
H	TGCGCTACCCCATCGTCACACCCAGCCAGCGCTGTGGTGGGGCTTGCCCTGGTGTCAAGACTCTCTTCCT					
M	TGCGCTATCCCATCATCACACCCAGCCAACGCTGTGGGGCGGCTGCCAGGAGTCAAGACCCCTCTTCCT					
1080	1090	1100	1110	1120	1130	1140
1180	1190	1200	1210	1220	1230	1240
H	CTTCCCCAACAGACTGGCTTCCCCAATAAGCACACGCCGCTTCAACGTCTACTGCTTCCGAGACTCGGC					
M	CTTCCCCAACAGACTGGCTTCCCCAGCAAGCAGAACCGCTTCAATGTCTACTGCTTCCGAGACTCTGCC					
1150	1160	1170	1180	1190	1200	1210
1250	1260	1270	1280	1290	1300	1310
H	CAGCCTTCTGCCATCCCTGAGGCCTCCAACCCAGCCTCCAACCCAGCCTCTGATGGACTAGAGGCTATCG					
M	CATCCCTCTGCTTCCCTCTGAGGCCTCTAGCCCAGCCTC-----AGATGGACTTGAGGCCATTG					
1220	1230	1240	1250	1260	1270	
1320	1330	1340	1350	1360	1370	1380
H	TCACAGTGACAGACCCCTGGAGGAACCTGCAGCTGCCCTCAGGAAGCCACAGAGAGTGAATCCCCGTGGGGC					
M	TCACAGTGACAGAAAGCTGGAGGAACCTGCAGCTGCCCTCAGGAAGCGATGGAGAGCGAGTCTCGTGGGGC					
1280	1290	1300	1310	1320	1330	1340

Fig. 240

1390	1400	1410	1420	1430	1440	1450
H	CATCTACTCCCATCCCATCATGGAGGACGGAGGGTGGAAGCTCCACTCCAGAAGACCCAGCAGAGGCC					
	::::::::::::::::	::::::::::::::::	::::::::::::::::	::::::::::::::::	::::::::::::::::	::::::::::::::::
M	CATCTACTCCCATCCCATCTCAGAAAGATGGGGGAGGAGGAAGCTCCACCCAGAAAGACCCAGCAGAGGCC					
1350	1360	1370	1380	1390	1400	1410
1460	1470	1480	1490	1500	1510	1520
H	CCTAGGACGCTCCTAGAAATTGAAACACAATCCATGGTACCGCCACGGGGTTCTCAGAAAGAGGAAGGTA					
	::::::::	::::::::	::::::::	::::::::	::::::::	::::::::
M	CCCAGGACTCCGCTAGAAATCGGAAACCCAATCCATTCGACCACTACCGAGTCCCTCAGAAAGAGGAAGCGG					
1420	1430	1440	1450	1460	1470	1480
1530	1540	1550	1560	1570	1580	1590
H	AGGCATTGGAGGAAGAGAAATATGAAGATGAAGAAGAGAGGAGGAAGAAGAGAGGAGAGGT					
	::::	::::	::::	::::	::::	::::
M	TAGCCCTGGAGGAAGAAAGATTCAAAGAC-----TTGGAGGCTCTGGAGGAAGAGAAAGGAGCA					
1490	1500	1510	1520	1530	1540	
1600	1610	1620	1630	1640	1650	1660
H	GGAGGATGAGGCTCTGTGGGCATGGCCCCAGCGAGCTCAGCAGCCCCGGCCCTGAGGCCCTCTCTCCCCACT					
	:::::	:	:::::	:::::	:::::	:::::
M	GGAGGA-----C-CTGTGGGTGTGGCCCCAGAGAGCTCAGCAGCCCC-----TCTCCCTACT					
1550	1560	1570	1580			1590
1670	1680	1690	1700	1710	1720	
H	GAGCCAGCAGCCAGGAGAAGTCACTCTCCAGG-----CGCCAGCAAGGGCAGTCTCTGCAGCCTGGTG					
	::	:::	:	:::::	:::::	:::::
M	GGCTCAGAAAC---AGAGCATTCACTCTCCAGGTGTCCCAACCCAGCCAGGCAAGTTCTACAGCTGGATG					
1600	1610	1620	1630	1640	1650	1660

Fig. 24P

```

1730      1740      1750      1760      1770      1780      1790
H CATCACCACTTCCTGATGGAGAGTCAGAAAGCTTCCAGGCCTCCAAGGTCCATGGACCACCTACTGAGAC
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M CGTCACCTTCTCCTG-----GGCCTCCAAGGTTCCGTGGACCGCCTGCAGAGAC
1670      1680      1690      1700      1710

1800      1810      1820      1830      1840      1850      1860
H TCTGCCCACTCCAGGAGAGGAACCTAGCATCCCCATCACCTTCCACTCTGGTTGAGGCAAGAGAGGTG
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M TTTGCTCCCCCGAGGGAGTGAGC-----GCCACATCTACT-CC----TGGT-GGGGCAAGAGAAAGTA
1720      1730      1740      1750      1760      1770

1870      1880      1890      1900      1910      1920      1930
H GGGGAGGCAACTGGTGGTCCCTGAGCTATCTGGGGTCCCTCGAGGAGAGAGCGAGAGACAGGAAGCTCC-
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M GGGGGGAAACTGGGAGCCCTGAGCTCTCTGGGGTTCTCTCGA---GAGAGCGAGGAGGCGAGGAGCTCCA
1780      1790      1800      1810      1820      1830

1940      1950      1960      1970      1980      1990      2000
H ----GAGGGTGCCCCCTTCCCTGCTTCCAGCCACACGGGCCCCCTGAGGGTACCAGGGAGCTGGAGGCCCC
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M GCTTGAGGATGGCCCCCTTCCCTACTTCCAGCTACATGGGCCCCCTGTGGGTCCCAGGGAGCTGGAGACCCC
1840      1850      1860      1870      1880      1890      1900

2010      2020      2030      2040      2050      2060      2070
H CTCTGAAGATAATTCTGGAAGAACTGCCCCAGCAGGGACCTCAGTGCAGGCCCCAGCCAGTGCTGCCCCACT
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M CTCAGAAGAGAGTCTGGAAGAACTGTCTTGGCAGGCACCTCAGTGCAGGCCCCAGCCAGTGCTGCCCCACC
1910      1920      1930      1940      1950      1960      1970

```

Fig. 24Q

```

2080      2090      2100      2110      2120      2130
H GACAGCGCCAGCCGAGGTGGAGTGGCCCGTGGTCCCGCATCAGGTAATT-----CTGCCCAAGGCTCA
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M GACAGTGCCAGCCACGGTGGAGTGGCTGTGGCTCCCTCATCAGGTGACTGTATCCCCAGGCCCTGCCCACA
1980      1990      2000      2010      2020      2030      2040

2140      2150
H A-----C-TGC-----CCTCT--CTAT-----CCTA-CT-----CCT
   : : : : : : : : : : : : : : : : : : : : : : : : : : :
M ATGGTGGACATGCTTGGAGGAGAGGAGGTTTCGCTGCCTATGTTGCCAGGCTATGGGGGGACCT
2050      2060      2070      2080      2090      2100      2110

2160      2170      2180      2190      2200
H TTTC-----TTCCC--C-----CTGCAGCTCTGG-----GTC--ACCTGA--CCTG----TAGTCCTTT
   : : : : : : : : : : : : : : : : : : : : : : : : : : :
M GTGCGATGTGGCCCTTCATTTCTGCAGCCCCGTGGCTGGAGGCCTTCCAGGAGCCTGCTACAAGCACTTT
2120      2130      2140      2150      2160      2170      2180

2210      2220      2230
H AACCCAC-----CA-----TCA-TCCCAAACCTCT-----C----CTGTCC----TTT
   . : : : : : : : : : : : : : : : : : : : : : : : : : :
M TCCACACGAAGGAGTTGGGAGGAGGCAGAAAGTCAGTGCCGAGCGCTAGGTGCTCATCTGACCAGCATCT
2190      2200      2210      2220      2230      2240      2250

2240      2250      2260      2270
H GC-----CT-----TCATTCTCT-TACCC---ACC---TCTACCTATGGGT-----CTC-----
   : : : : : : : : : : : : : : : : : : : : : : : : : :
M GCACCCCTGAGGAGCAAGACTTTGTCAATGATCGATACCGGGAGTACCAGTGGATTGGGCTCAATGACAG
2260      2270      2280      2290      2300      2310      2320

```

Fig. 24R

```

2280                2290        2300        2310        2320
H  --CAATCTCGGATATCCAC-----CTTGTGG-GTATCTCAGCTCTCCGCGT-CTT-TACCCCTGTG-AT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M  GACCATCGAGGGTGACTTCTTGTGGTCAGATGGTGCCCTCTGCTCTATGAAAACTGGAACCCCTGGGCAG
2330      2340      2350      2360      2370      2380      2390

2330                2340                2350
H  CC----CAGC-----CCCGCC-----ACTG-----ACCA---TCGTGA-----
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M  CCTGACAGCTACTTCCTGTCTCTGGGAGAACTGTGTGGTCATGGTGGCATGACCAGGACAGTGGAGTG
2400      2410      2420      2430      2440      2450      2460

2360      2370      2380                2390
H  ----CCCTTCC-CTGCCATTGGGCC--CTCCA-----CCTGTGG--CTCACATCTC
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M  ATGTGCCCCTGCAACTACCATCTATCCTACACCTGCAAGATGGGGCTTGTGTCTCCTGTGGGCCTC-CACCAC
2470      2480      2490      2500      2510      2520      2530

2400      2410      2420      2430      2440      2450
H  GCCAGCCCCA----CA-----GAGCATCCTCAG---GCCCTCTCCAAGGTCCTCATCACCTATTGCA
      . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M  AGCTACCCCTGGCTCAAATATTGTGTCGCCCTCGGCTGCGCTACGCGGTGGATACTGTGCTTCGATATCG
2540      2550      2560      2570      2580      2590      2600

2460                2470      2480
H  --GCCTT--CAGG---GCTCGGC-----CTATTTTCCACTAC-----TCC
      : : : . : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M  ATGCCGAGACGGGCTGGCTCAGCGCAACCTGCCGTTGATCCGCTGCCAGGAGAAATGGGCTTTGGGAGGCC
2610      2620      2630      2640      2650      2660      2670

```

Fig. 24S

```

2490      2500      2510      2520      2530
H CTTCA-TCCGCCGTGTGCC-----GTCC---CCTTTAGCTGC-CTCCT-----ATTGATCTC
: : : . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M CCTCAGATTTCCTGTGTACCCCGGAGGCCCTGGCCGTGCTCTGCGCTCCATGGACGCCCCAGAGGACCAC
2680      2690      2700      2710      2720      2730      2740

2540      2550      2560      2570      2580
H AGGA-AGC-----CTGGGAGTC-CC-TTCTCACC--CCTC-AACCTCCGGAGT-CCAGGAGAAC
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M GGGACAGCTCTCGAGGCACAGGAAGCACCCGTTGACACCCGCTCCAGTCTCTAGGAGCCTGGAAGAC
2750      2760      2770      2780      2790      2800      2810

2590      2600      2610      2620      2630
H CCGTACCCCCA-CAGAGCCTTAA-GCAACTACT-----TCT-----GTGAAGTATTT
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M TGCTGCCCCCAGCAGGACCCTCTCACATCAACTGCCAGTGCTCTTCCCCATGATAGGGGTGACGTGAGA
2820      2830      2840      2850      2860      2870      2880

2640      2650
H ----TTGACTGT--TTCA-----TGGAACA-----
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M GGGTGGGACTGAAATTTCAGAGGACAGCGCTCGAAGGGGTTTCTGGGAAACACTTGGGTGGCTCCGCCCC
2890      2900      2910      2920      2930      2940      2950

2660      2670      2680
H -----AGCCTTGGAAAT-----AAATCTCTATTAA-----AC
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M CTCACACAAGGGCCTCAGGTTTACCCGGTAAGTCCCTAAGTGCCTCAACTGCCCTCTCATGTCAGCTGC
2960      2970      2980      2990      3000      3010      3020

```

Fig. 24T

```

H CGCTTTGT-----AAC-----CAAAAAAAAAAAAAAA
: : : : :
M CTCCTTGTCCCTCGATNTCGTNAGGGGACACTGTGCTATTTCGATCCTTGATTTGTCGAAGAGTTTTAGGAT
3030 3040 3050 3060 3070 3080 3090

2710
H AAA-----AAAAAAGGCGG--CC-----GC
: : : : :
M GGAGTACCAGCAAAACCAGGTGGAAATAAAGTTGTCTGAACCCCAAAGAAAAAAA
3100 3110 3120 3130 3140 3150

```

Fig. 24U

	M	A	P	P	A	A	R	L	A	L	L	11
GTCGACCCACGCGTCCGCCACGCGTCCGGCCC	ATG	GCG	CCG	CCC	GCC	GCC	GCG	CTC	GCC	CTG	CTC	66
S	A	A	A	L	T	L	A	A	R	P	A	31
TCC GCC GCG GCG CTC	ACG	CTG	GCG	GCC	CGG	CCC	GCG	CCT	AGC	CCC	GCG	126
P	E	C	F	T	A	N	G	A	D	Y	R	51
CCC GAG TGT TTC	ACA	GCC	AAT	GGT	GCG	GAT	TAT	AGG	GGA	ACA	CAG	186
Q	G	G	K	P	C	L	F	W	N	E	T	71
CAA GGC GGG AAG CCA	TGT	CTG	TTT	TGG	AAC	GAG	ACT	TTC	CAG	CAT	CCA	246
K	Y	P	N	G	E	G	L	G	E	H	N	91
AAA TAC CCC AAC	GGG	GAG	GGG	GCG	CTG	GGT	GAG	CAC	AAC	TAT	TGC	306
D	V	S	P	W	C	Y	V	A	E	H	E	111
GAC GTG AGC CCC	TGG	TGC	TAT	GTG	GCA	GAG	CAC	GAG	GAT	GGT	GTC	366
E	I	P	A	C	Q	M	P	G	N	L	G	131
GAG ATA CCT GCT	GCT	TGC	CAG	ATG	CCT	GGA	AAC	CTT	GGC	TGC	TAC	426
P	P	L	T	G	T	S	K	T	S	N	K	151
CCT CCT CTA	ACT	GGC	ACC	AGT	AAA	ACG	AAA	CTC	TCC	AAC	AAA	486
F	C	R	S	Q	R	F	K	F	A	G	M	171
TTT TGT CGG	AGT	CAG	AGG	TTC	AAG	TTT	GCT	GGG	ATG	GAG	TCA	546

Fig. 25A

G	N	N	P	D	Y	W	K	Y	G	E	A	A	S	T	E	C	N	S	V	191
GG	A	A	A	T	C	C	T	G	A	T	T	G	G	G	G	A	G	A	A	606
C	F	G	D	H	T	Q	P	C	G	G	D	G	R	I	I	L	F	D	T	211
T	G	C	T	T	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	666
L	V	G	A	C	G	G	N	Y	S	A	M	S	S	V	V	Y	S	P	D	231
C	T	C	T	G	C	T	G	T	T	C	A	T	T	T	T	T	T	T	T	726
F	P	D	T	Y	A	T	G	R	V	C	Y	W	T	I	R	V	P	G	A	251
T	T	C	C	C	A	C	C	C	C	C	C	C	C	C	C	C	C	C	C	786
S	H	I	H	F	S	F	P	L	F	D	I	R	D	S	A	D	M	V	E	271
T	C	C	A	T	C	T	T	C	T	T	T	T	T	T	T	T	T	T	T	846
L	L	D	G	Y	T	H	R	V	L	A	R	F	H	G	R	S	R	P	P	291
C	T	T	C	T	T	C	C	C	C	C	C	C	C	C	C	C	C	C	C	906
L	S	F	N	V	S	L	D	F	V	I	L	Y	F	F	S	D	R	I	N	311
C	T	G	T	T	C	T	C	T	T	C	T	T	T	T	T	T	T	T	T	966
Q	A	Q	G	F	A	V	L	Y	Q	A	V	K	E	E	L	P	Q	E	R	331
C	A	G	C	C	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	1026

Fig. 25B

P	A	V	N	Q	T	V	A	E	V	I	T	E	Q	A	N	L	S	V	S	351
CCC	GCT	GTC	AAC	CAG	ACG	GTG	GCC	GAG	GTG	ATC	ACG	GAG	CAG	GCC	AAC	CTC	AGT	GTC	AGC	1086
A	A	R	S	S	K	V	L	Y	V	I	T	T	S	P	S	H	P	P	Q	371
GCT	GCC	CGG	TCC	TCC	AAA	GTC	CTC	TAT	GTC	ATC	ACC	ACC	AGC	CCC	AGC	CAC	CCA	CCT	CAG	1146
T	V	P	G	S	N	S	W	A	P	P	M	G	A	G	S	H	R	V	E	391
ACT	GTC	CCA	GGT	AGC	AAT	TCC	TGG	GCG	CCA	CCC	ATG	GGG	GCT	GGA	AGC	CAC	AGA	GTT	GAA	1206
G	W	T	V	Y	G	L	A	T	L	L	I	L	T	V	T	A	I	V	A	411
GGA	TGG	ACA	GTC	TAT	GGT	CTG	GCA	ACT	CTC	CTC	ATC	CTC	ACA	GTC	ACA	GCC	ATT	GTA	GCA	1266
K	I	L	L	H	V	T	F	K	S	H	R	V	P	A	S	G	D	L	R	431
AAG	ATA	CTT	CTG	CAC	GTC	ACA	TTC	AAA	TCC	CAT	CGT	GTT	CCT	GCT	TCA	GGG	GAC	CTT	AGG	1326
D	C	H	Q	P	G	T	S	G	E	I	W	S	I	F	Y	K	P	S	T	451
GAT	TGT	CAT	CAA	CCA	GGG	ACT	TCG	GGG	GAA	ATC	TGG	AGC	ATT	TTT	TAC	AAG	CCT	TCC	ACT	1386
S	I	S	I	F	K	K	K	L	K	G	Q	S	Q	Q	D	D	R	N	P	471
TCA	ATT	TCC	ATC	TTT	AAG	AAG	AAA	CTC	AAG	GGT	CAG	AGT	CAA	CAA	GAT	GAC	CGC	AAT	CCC	1446
L	V	S	D	*																476
CTT	GTG	AGT	GAC	TAA																1461

Fig. 25C

AAACCCCACTGTGCCCTAGGACTTGAGGTCCCTCTTTGAGCTCAAGGCTGCCGTGGTCAACCTCTCCTGTGGTTCTTCTC 1540
TGACAGACTCTTCCCTCCTCTCCCTCTGCCCTCGGCCCTCTTCGGGGAAACCCCTCCTTACAGACTAGGAAGAGGCACCT 1620
GCTGCCAGGGCAGGCAGAGCCCTGGATTCCCTCCCTGCTT 1657

Fig. 25D

GTCGACCCACGGTCCGCGCTCCCGGTGCTCCCGCTGCCCCCTCTGCCCCGGCGCCCGGGGTCCCGCACTGACGGCC															79					
M	A	P	P	A	A	R	L	A	L	L	S	A	A	A	L	T	L	A	19	
C	ATG	GCG	CCG	CCC	GCC	CGT	CTC	GCG	CTG	CTC	TCC	GCC	GCT	GCG	CTC	ACT	CTG	GCG	137	
A	R	P	A	P	G	P	R	S	G	P	E	C	F	T	A	N	G	A	D	39
GCC	CGG	CCC	GCG	CCC	GGT	CCC	CGC	TCC	GGC	CCC	GAG	TGC	TTC	ACA	GCC	AAC	GGT	GCA	GAT	197
Y	R	G	T	Q	S	W	T	A	L	Q	G	G	K	P	C	L	F	W	N	59
TAC	AGG	GGA	ACA	CAG	AGC	TGG	ACA	GCG	CTG	CAA	GGT	GGG	AAG	CCA	TGT	CTG	TTC	TGG	AAC	257
E	T	F	Q	H	P	Y	N	T	L	K	Y	P	N	G	E	G	G	L	G	79
GAG	ACT	TTC	CAG	CAT	CCG	TAC	AAC	ACG	CTG	AAG	TAC	CCC	AAC	GGG	GAA	GGA	GGA	CTG	GGC	317
E	H	N	Y	C	R	N	P	D	G	D	V	S	P	W	C	Y	V	A	E	99
GAG	CAC	AAT	TAT	TGC	AGA	AAT	CCA	GAT	GGA	GAC	GTG	AGC	CCT	TGG	TGC	TAC	GTG	GCC	GAG	377

Fig. 25E

H	E	D	G	V	Y	W	K	Y	C	E	I	P	A	C	Q	M	P	G	N	119
CAT	GAG	GAC	GGA	GTC	TAC	TGG	AAG	TAC	TGT	GAA	ATT	CCT	GCC	TGC	CAG	ATG	CCT	GGA	AAC	437
L	G	C	Y	K	D	H	G	N	P	P	P	L	T	G	T	S	K	T	S	139
CTT	GGC	TGC	TAC	AAG	GAT	CAT	GGA	AAC	CCA	CCT	CCT	CTC	ACG	GGC	ACC	AGT	AAA	ACC	TCT	497
N	K	L	T	I	Q	T	C	I	S	F	C	R	S	Q	R	F	K	F	A	159
AAC	AAG	CTC	ACC	ATA	CAA	ACC	TGT	ATC	AGC	TTC	TGT	CGG	AGT	CAG	AGA	TTC	AAG	TTT	GCT	557
G	M	E	S	G	Y	A	C	F	C	G	N	N	P	D	Y	W	K	H	G	179
GGG	ATG	GAG	TCA	GGC	TAT	GCC	TGC	TTC	TGT	GGG	AAC	AAT	CCT	GAC	TAC	TGG	AAG	CAC	GGG	617
E	A	A	S	T	E	C	N	S	V	C	F	G	D	H	T	Q	P	C	G	199
GAG	GCG	GCC	AGC	ACC	GAG	TGC	AAT	AGT	GTC	TGC	TTC	GGG	GAC	CAC	ACG	CAG	CCC	TGC	GGT	677
G	D	G	R	I	I	L	F	D	T	L	V	G	A	C	G	G	N	Y	S	219
GGG	GAC	GGC	AGG	ATT	ATC	CTC	TTT	GAC	ACT	CTC	GTG	GGC	GCC	TGC	GGT	GGG	AAC	TAC	TCA	737
A	M	A	A	V	V	Y	S	P	D	F	P	D	T	Y	A	T	G	R	V	239
GCC	ATG	GCA	GCC	GTG	GTG	TAC	TCC	CCT	GAC	TTC	CCT	GAC	ACC	TAC	GCC	ACT	GGC	AGA	GTC	797
C	Y	W	T	I	R	V	P	G	A	S	R	I	H	F	N	F	T	L	F	259
TGC	TAC	TGG	ACC	ATC	CGG	GTT	CCA	GGA	GCC	TCT	CGC	ATC	CAT	TTC	AAC	TTC	ACC	CTG	TTT	857
D	I	R	D	S	A	D	M	V	E	L	L	D	G	Y	T	H	R	V	L	279
GAT	ATC	AGG	GAC	TCT	GCA	GAC	ATG	GTG	GAG	CTG	CTG	GAC	GGC	TAC	ACC	CAC	CGC	GTC	CTG	917

Fig. 25F

V	R	L	S	G	R	S	R	P	P	L	S	F	N	V	S	L	D	F	V	299
GTC	CGG	CTC	AGT	GGG	AGG	AGC	CGC	CCG	CCT	CTG	TCT	TTC	AAT	GTC	TCT	CTG	GAT	TTT	GTC	977
I	L	Y	F	F	S	D	R	I	N	Q	A	Q	G	F	A	V	L	Y	Q	319
ATT	TTG	TAT	TTC	TTC	TCT	GAT	CGC	ATC	AAT	CAG	GCC	CAG	GGA	TTT	GCT	GTG	TTG	TAC	CAA	1037
A	T	K	E	E	P	P	Q	E	R	P	A	V	N	Q	T	L	A	E	V	339
GCC	ACC	AAG	GAG	GAA	CCG	CCA	CAG	GAG	AGA	CCT	GCT	GTC	AAC	CAG	ACC	CTG	GCA	GAG	GTG	1097
I	T	E	Q	A	N	L	S	V	S	A	A	H	S	S	K	V	L	Y	V	359
ATC	ACC	GAG	CAA	GCC	AAC	CTC	AGT	GTC	AGC	GCT	GCC	CAC	TCC	TCC	AAA	GTC	CTC	TAT	GTC	1157
I	T	P	S	P	S	H	P	P	Q	T	A	Q	V	A	I	P	G	H	R	379
ATC	ACC	CCC	AGC	CCC	AGC	CAC	CCT	CCG	CAG	ACT	GCC	CAG	GTA	GCC	ATT	CCT	GGG	CAC	CGT	1217
Q	L	G	P	T	A	T	E	W	K	D	G	L	C	T	A	W	R	P	S	399
CAG	TTG	GGG	CCA	ACA	GCC	ACA	GAG	TGG	AAG	GAT	GGA	CTG	TGT	ACG	GCC	TGG	CGA	CCC	TCC	1277
S	S	S	Q	S	Q	Q	L	S	Q	R	F	F	C	M	S	H	L	N	L	419
TCA	TCC	TCA	CAG	TCA	CAG	CAG	TTG	TCG	CAA	AGA	TTC	TTC	TGC	ATG	TCA	CAT	TTA	AAT	CTC	1337
I	E	S	L	H	Q	E	T	L	G	T	V	V	S	L	G	L	L	E	I	439
ATC	GAG	TCC	CTG	CAT	CAG	GAG	ACC	TTA	GGG	ACT	GTC	GTC	AGC	CTG	GGG	CTT	CTG	GAG	ATA	1397
S	G	P	F	S	M	N	L	P	L	Q	S	P	S	L	R	R	S	S	R	459
TCT	GGA	CCA	TTT	TCT	ATG	AAC	CTT	CCA	CTA	CAA	TCT	CCA	TCT	TTA	AGA	AGA	AGC	TCA	AGG	1457

Fig. 25G

V R V N K M T A I P S *
 GTC AGA GTC AAC AAG ATG ACC GCA ATC CCC TCG TGA 471
 1493

GTGACTGAAGCCACGCCCTGCATGAGAGGCTCCGCTCCAAGCTCGAGTTTGCTCCCCTGAGTTCTCCTCTGATGAGTTC 1572
 CCTGCCCTCCCATTCACCAACCATCTCTTTTGGAGACACCCTGTCTTTAGAGGCAGCCAGCCTGGGATCCTCCATCACAT 1651
 GTACCAGCCCTGGCTGCTCTGCTGGGGATGGTAAGACAGGCCCCAGGCTGACAGGACACAGCTGGACCTGACTCCAGAAGA 1730
 CTC'TTGGGTGGTGGGAGGTATAGTGTAGGATGAGTTTCTTCTGCTCTCTCTGTTTGTCCACATACAGATCGGTTTC 1809
 CCCGTGCTTTACAGTTTGCAATAGAGCCAGACTGAAGAAGTGTGAGGTTTCTAGGCTGGCCTGGTTCCTCCACTAAGA 1888
 GTGGCATTTGGCGCCCTAGAGGCCACAGAGGCCAGTGTAGGCTTTGAGCTTTCTCTGCTGCCAACTACCATGTGTCACTT 1967
 AGTCCGAGGGGACTGAGAGCAGGGCCACACCAGATGTCATCTTTCTAGAGGGTTCTTTTAGTACCCACTGACCAATGG 2046
 GGCAAGCCTGAGGATTGGTCCATCTGTTTGTCCATGGAACAGACACAGTGAACCTTCCCTGGATACTAGACTTAAC TAGCC 2125
 TAGCCCTCAAGTAGTTGCCAATCCTGTGGAATCAGAAATTCAGCCTGTCTTCTGCTCAGCCCCAAGCCTGTAGCCCTAG 2204
 AGCTGGGGCTGTAGCCTAGAGCTGGGGCTGTAGCCTAGAGCTGGGGCTGTAGCACAGAGCTGGGGCTGTAGCCTAGAGC 2283
 TGGGGCTGTAGCACAGAGCTGGGGCTGTAGCCTAGAGCTGGGGCTGTAGCACAGAGCTGGGGCTGTAGCACAGAGCTGG 2362
 GGCTGTAGCCTAGAGCTGGGGCTGTAGCACAGAGCTGGGGCTGTAACTCAGCGATCAAGAGCTTGCTTTGTATACATCG 2441
 GACCCTAGGTTCTATCCCAGCACTATCAGAAAGGTGGGAGAGAAAAGACTGCACCATAGCATGCGGGCAGCATCTGTGG 2520
 TTCCCTACGTGAGGTGTCATCATTTTAAAGCAGATCAAACACTACCCGCGAGTTTGTCCCTTTGTCCCTTATCATGGGAGC 2599
 AGAGTAGGAGTAAGGGCTCTGGTCTTGCTCATTTGTCCCCAGACAGGGAGGCAAGGAAAGGTGAGGCTTGGAACTGGA 2678
 GATCCTCCAGGAAAGCTGCAAGATTGAGAGACCCAGCTGCAGTTGGGAGAGGAAGGGCCATCCCCGACTGAGAAAGTC 2757
 CTGCAGTCTGGAAGTGGCCCTTTGTTCAGCAGCAGCTGTGCCCTGAAGGTAGACCTTGGTCACCTCTCCTGCCAGCCCTGA 2836
 GCCCTGCTCTCCTGGGTACCCCTCCCTGGAACACCATGCTAACCTTCCCCGAGTCTCTCAGTCACTGCCATTGAGGCCCTC 2915
 TCCTCTAGCTGCTGCCAGGACTGTCTGGGGCCATCTGGGGATCAGGGAGAGGCAGGAGTACTGACGAGGCAG 2994
 TGACCTGAGCTGATGAGTCAACCAGAGGACACAGAGTCTACAGTGGGCTGGCTGCTGCTCAGCTCCCTATGGGAGGCC 3073
 TACAGGGGTACTAAGCTAGGGGTTCATCTCATTTGATCTGGGAAAGGCTACAGGCTCCTGGATGTGAAGACAGGCC 3152
 CACTACATAAGAAGACCACCTGGAAATAGACTGACAGGAGCAGGTTCCACTCTAGGCTGTCCATAGCGTTTTCAGGAGCTC 3231

Fig. 25H

CCCTGAGACCAAGTGTGAGTCACAGAGTGCCATGTGCGTAGTGCAATAAAGGATATGGGTTCTTAACCCAGGGAAGGCTC 3310
 ATAGCAGGCCAGGACATTTTTCAGCTCAGAGCACTGGCCCCAGGCTTCCTCTAAGCCACCACCTCACCCTGTCTCTTCCCT 3389
 ATCTCGGACACAGGAAGCAAGCCCAAGTGTGGTGGCAGCTGCGGCTCAGCATTTGGTGTCCCCAGGAAGGCGGTGGATG 3468
 TGCCACGCTCCTTTTGTCTGTGGCCCTGGCACAGCCCAACACTGCAGGGCCCACTTCTCTCTTGGGGGTAGGGACAC 3547
 ATAAGGAATAAATAACCCACCTCCAACAACAGCAGAGAGACAGTGGGAAGGAGGCTGTAAATCACCCAGGCCAGACCTC 3626
 CAGAAATGACAGGCACAGTCTGTAGAACCTGTAGGCAGCCAGTCAAGAGGGCCCTTTGTGCTGGTAACACCCCTGCCCTG 3705
 GAGCATAGGGGTAAAGCCGAGGGAAGAGCAGCCCTCAGAGACATCAGCTAAATAAATAGGTGCCCTATGTCCCTCCCT 3784
 TCCTGTACACTGCTTACAAAGCAGAGACAGAGAGCTCTGGACTTCTCTAAATGTGGGCTCTGGCTTCAGACTCCTCAGCCA 3863
 GCGGCTGCCCTAAAGTGAGCAAGGAGAACAGAGCTCTGGACTTCTCTAAATGTGGGCTCTGGCTTCAGACTCCTCAGCCA 3942
 AAAGCTCTTGAAAGATCAAGCTCTGGCGGGTACAGCTGTCTGGCCGTGGCCAGCCCATGGGATGTGCCGTGGGCCAG 4021
 GTGCCACCCACGGCTCACTGTCAATCCAGGAGGACCCACCTGATGCTCCTCATCATCCGCTGGCTGACACTATCA 4100
 GAGCTCGCGCGGCTGTGCCAGGACAGACTGACTACACTTGACCTTCAAGAGCACTTAGAAGTGGATGGCCTCCAGA 4179
 CTCGTCAAGCCCTCGCAGGGCCACACAAGTCTCCCGAGCCAAAGTCCACAAGCCTCCATGGTTCCCTGGCTCCTCCT 4258
 GTGGAGTGTCTCTGTGATGTCTGAGGTCGTCTTTGGGTACCCGCCCTGGGAACCTGCTAACCTCCGATTGGTCCCTTTGT 4337
 GTCCTCTGTTTACTGTCTCTTCTACCTCCAGGTCACTTAGCTCTGGCTGTCTGGCTGGAGTGGGGGTGGGGATGCT 4416
 GGCTGCACCCCAACCTGGTCTGCCAACAGAACCTGGGGGCTCACACGGGCTCCTGTCTTGCCAAAGCTGGAGCTGAGC 4495
 AACTGGCCCAAGGCTGAGTGGGGCAGAGCAAAACAAGTGGGAAGGGATCTCTCTCCTTAGAGGGAGGTGCCCAAGGTGT 4574
 AGATCCAGCGAGGAGCTGCCATCCCCGCCACCTTCATAGCAGCAAGACCTTCCCATTTCCAAATCTCACCTCCAGCAG 4653
 GGATATGACTTTGGACACAAGGCTTTATTTGTAAATATGCTCTTAAATATGCAACTTTTGAGAAATAAGATAGAAACATCA 4732
 TGTAATTTTAAATAATAAAATGAAGTGTGACACACTGTATACAATTTAAATATATATATATTTTGTAGGATTTTGTATTAAGAA 4811
 AATGGAATGTGATGGTACTTAACCTTTTACAAAAGAGAGAAAATGTTATTTTACTGTTTGAAAGAAAATAAATATTCTCA 4890
 TTGTTGTAGAAAAAATAAAAAAAGGGGCGCGC 4928

Fig. 25I

Hum.	MAPPAARLALLSAAALTLAARPAPSPGLGPGPECF	TANGADYRG	TQNW	TALQG	KPCLFW	NETFQHPYNT	
	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	
Mur.	MAPPAARLALLSAAALTLAARPAPGPR--	SGPECF	TANGADYRG	TQSW	TALQG	KPCLFW	NETFQHPYNT
	10	20	30	40	50	60	
Hum.	LKYPNGEGGLGEHNYCRNPDGDVSPWCYVAEHEDGVYWKYCEI	PACQ	MPGN	LG	CYKDHGN	PPPLTG	TGTSKT
	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	
Mur.	LKYPNGEGGLGEHNYCRNPDGDVSPWCYVAEHEDGVYWKYCEI	PACQ	MPGN	LG	CYKDHGN	PPPLTG	TGTSKT
	70	80	90	100	110	120	130
Hum.	SNKLTIQTCISFCRSQRKFAGMESGYACFCGNNPDYWKYGEAA	STECN	SVCF	GDHTQ	PCGGD	GRIIL	FD
	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	
Mur.	SNKLTIQTCISFCRSQRKFAGMESGYACFCGNNPDYWKHGEAA	STECN	SVCF	GDHTQ	PCGGD	GRIIL	FD
	140	150	160	170	180	190	200
Hum.	TLVGACGGNYSAMSSVVYSPDFPDTYATGRVCYWTIRVPGASHIH	FSFPL	FDIR	SADM	VELLD	GYTHRV	
	220	230	240	250	260	270	280
Mur.	TLVGACGGNYSAMAAVVYSPDFPDTYATGRVCYWTIRVPGASRIH	FNFTL	FDIR	SADM	VELLD	GYTHRV	
	210	220	230	240	250	260	270

	290	300	310	320	330	340	350
Hum.	LARFHGRSRPPLSFNVSLDFVILYFFSDRINQAQGFVLYQAVKEELPOERP AVNQTVAEVITEQANLSV						
	:::	:::	:::	:::	:::	:::	:::
Mur.	LVRLSGRSRPPLSFNVSLDFVILYFFSDRINQAQGFVLYQATKEEPPQERP AVNQTLAEVITEQANLSV						
	280	290	300	310	320	330	340
Hum.	SAARSSKVLVYTTPSPHPPTVPGSNSWAPPMGAGSHRVEGWTVYG L ATLLITVTAI VAKILLHVTFK						
	:::	:::	:::	:::	:::	:::	:::
Mur.	SAAHSSKVLVYTTPSPHPPTAQVAIPCHRQLGPTA---TEWKD-GLCTAWRPSSSSQS QLSQRFFCM						
	350	360	370	380	390	400	410
Hum.	SHRVPASGDLRDCHQPGTSGEIWSIFYKPSTISIFKKKLKGQSQ-QDDRNPLVSD						
	::	.	.	:	:	:	:
Mur.	SHLNLIESHQETLGTVVSLGLEISGPFMSMNLPLQSPSLRRS RVRVNKMTAIPS						
	420	430	440	450	460	470	

Fig. 25K

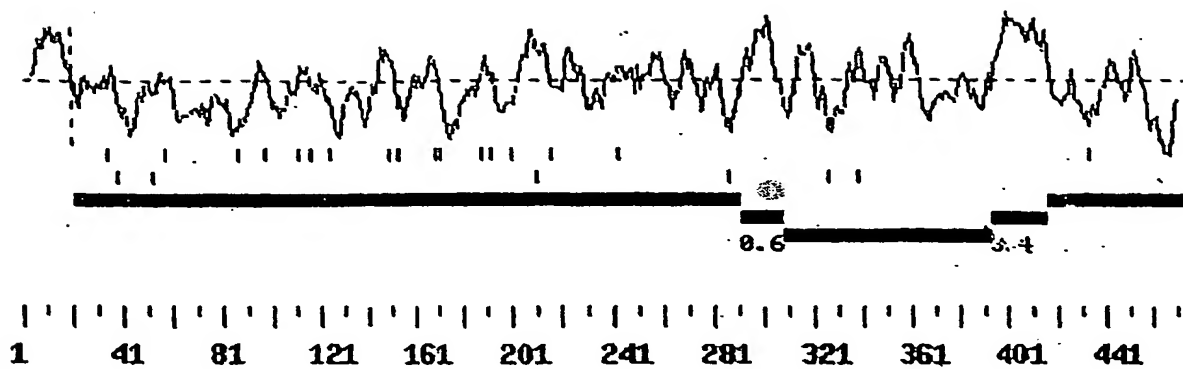


Fig 25L

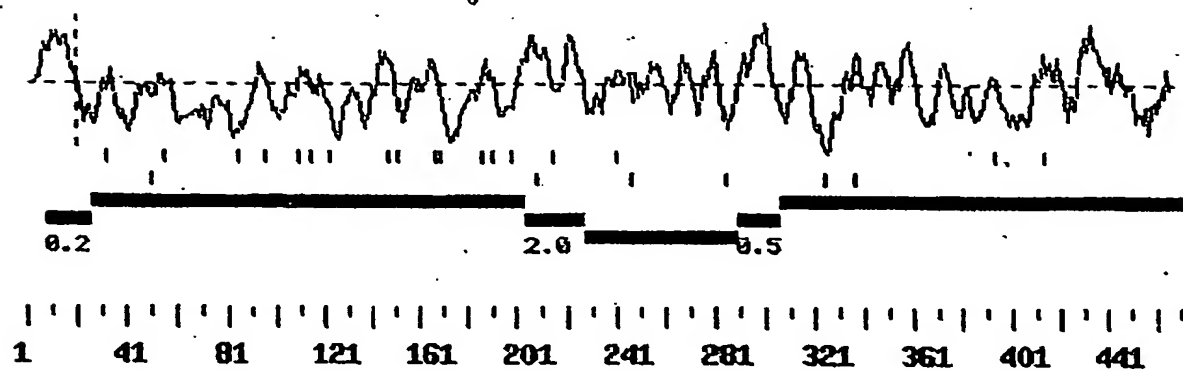


Fig. 25M

GCGGCCGCTCGCGATCTAGAACTAGTA	M	M	L	P	Q	N	S	W	H	I	D	F	G	13
ATG ATG CTG CCT CAA AAC TCG TGG CAT ATT GAT TTT GGA														66
R C C C H Q N L F S A V T C I L L L N														33
AGA TGC TGC TGT CAT CAG AAC CTT TTC TCT GCT GGT GTG GTA ACT TGC ATC CTG CTC CTG AAT														126
S C F L I S S F N G T D L E L R L V N G														53
TCC TGC TTT CTC ATC AGC AGT TTT AAT GGA ACA GAT TTG GAG TTG AGG CTG GTC AAT GGA														186
D G P C S G T V E V K F Q G Q W G T V C														73
GAC GGT CCC TGC TCT GGG ACA GTG GAG GTG AAA TTC CAG GGA CAG TGG GGG ACT GTG TGT														246
D D G W N T T A S T V V C K Q L G C P F														93
GAT GAT GGG TGG AAC ACT ACT GCC TCA ACT GTC GTG TGC AAA CAG CTT GGA TGT CCA TTT														306
S F A M F R F G Q Q A V T R H G K I W L D														113
TCT TTC GCC ATG TTT CGT TTT GGA CAA GCC GTG ACT AGA CAT GGA AAA ATT TGG CTT GAT														366
D V S C Y G N E S A L W E C Q H R E W G														133
GAT GTT TCC TGT TAT GGA AAT GAG TCA GCT CTC TGG GAA TGT CAA CAC CGG GAA TGG GGA														426
S H N C Y H G E D V G V N C Y G E A N L														153
AGC CAT AAC TGT TAT CAT GGA GAA GAT GTT GGT GTG AAC TGT TAT GGT GAA GCC AAT CTG														486

Fig. 26A

G	L	R	L	V	D	G	N	N	S	C	S	G	R	V	E	V	K	F	Q	173
GGT	TTG	AGG	CTA	GTG	GAT	GGA	AAC	AAC	TCC	TGT	TCA	GGG	AGA	GTG	GAG	GTG	AAA	TTC	CAA	546
E	R	W	G	T	I	C	D	D	G	W	N	L	N	T	A	A	V	V	C	193
GAA	AGG	TGG	GGG	ACT	ATA	TGT	GAT	GAT	GGG	TGG	AAC	TTG	AAT	ACT	GCT	GCC	GTG	GTG	TGC	606
R	Q	L	G	C	P	S	S	F	I	S	S	G	V	V	N	S	P	A	V	213
AGG	CAA	CTA	GGA	TGT	CCA	TCT	TCT	TTT	ATT	TCT	TCT	GGA	GTT	GTT	AAT	AGC	CCT	GCT	GTA	666
L	R	P	I	W	L	D	D	I	L	C	Q	G	N	E	L	A	L	W	N	233
TTG	CGC	CCC	ATT	TGG	CTG	GAT	GAC	ATT	TTA	TGC	CAG	GGG	AAT	GAG	TTG	GCA	CTC	TGG	AAT	726
C	R	H	R	G	W	G	N	H	D	C	S	H	N	E	D	V	T	L	T	253
TGC	AGA	CAT	CGT	GGA	TGG	GGA	AAT	CAT	GAC	TGC	AGT	CAC	AAT	GAG	GAT	GTC	ACA	TTA	ACT	786
C	Y	D	S	S	D	L	E	L	R	L	V	G	G	T	N	R	C	M	G	273
TGT	TAT	GAT	AGT	AGT	GAT	CTT	GAA	CTA	AGG	CTT	GTA	GGT	GGA	ACT	AAC	CGC	TGT	ATG	GGG	846
R	V	E	L	K	I	Q	G	R	W	G	T	V	C	H	H	K	W	N	N	293
AGA	GTA	GAG	CTG	AAA	ATC	CAA	GGA	AGG	TGG	GGG	ACC	GTA	TGC	CAC	CAT	AAG	TGG	AAC	AAT	906
A	A	A	D	V	V	C	K	Q	L	G	C	G	T	A	L	H	F	A	G	313
GCT	GCA	GCT	GAT	GTC	GTA	TGC	AAG	CAG	TTG	GGA	TGT	GGA	ACC	GCA	CTT	CAC	TTC	GCT	GGC	966
L	P	H	L	Q	S	G	S	D	V	V	W	L	D	G	V	S	C	S	G	333
TTG	CCT	CAT	TTG	CAG	TCA	GGG	TCT	GAT	GTT	GTA	TGG	CTT	GAT	GGT	GTC	TCC	TGC	TCC	GGT	1026

Fig. 26B

N	E	S	F	L	W	D	C	R	H	S	G	T	V	N	F	D	C	L	H	353
AAT	GAA	TCT	TTT	CTT	TGG	GAC	TGC	AGA	CAT	TCC	GGA	ACC	GTC	AAT	TTT	GAC	TGT	CTT	CAT	1086
Q	N	D	V	S	V	I	C	S	D	G	A	D	L	E	L	R	L	A	D	373
CAA	AAC	GAT	GTG	TCT	GTG	ATC	TGC	TCA	GAT	GGA	GCA	GAT	TTG	GAA	CTG	CGA	CTA	GCA	GAT	1146
G	S	N	N	C	S	G	R	V	E	V	R	I	H	E	Q	W	W	T	I	393
GGA	AGT	AAC	AAT	TGT	TCA	GGG	AGA	GTA	GAG	GTG	AGA	ATT	CAT	GAA	CAG	TGG	TGG	ACA	ATA	1206
C	D	Q	N	W	K	N	E	Q	A	L	V	V	C	K	Q	L	G	C	P	413
TGT	GAC	CAG	AAC	TGG	AAG	AAT	GAA	CAA	GCC	CTT	GTG	GTT	TGT	AAG	CAG	CTA	GGA	TGT	CCG	1266
F	S	V	F	G	S	R	R	A	K	P	S	N	E	A	R	D	I	W	I	433
TTC	AGC	GTC	TTT	GGC	AGT	CGT	CGT	GCT	AAA	CCT	AGT	AAT	GAA	GCT	AGA	GAC	ATT	TGG	ATA	1326
N	S	I	S	C	T	G	N	E	S	A	L	W	D	C	T	Y	D	G	K	453
AAC	AGC	ATA	TCT	TGC	ACT	GGG	AAT	GAG	TCA	GCT	CTC	TGG	GAC	TGC	ACA	TAT	GAT	GGA	AAA	1386
A	K	R	T	C	F	R	R	S	D	A	G	V	I	C	S	D	K	A	D	473
GCA	AAG	CGA	ACA	TGC	TTC	CGA	AGA	TCA	GAT	GCT	GGA	GTA	ATT	TGT	TCT	GAT	AAG	GCA	GAT	1446
L	D	L	R	L	V	G	A	H	S	P	C	Y	G	R	L	E	V	K	Y	493
CTG	GAC	CTA	AGG	CTT	GTC	GGG	GCT	CAT	AGC	CCC	TGT	TAT	GGG	AGA	TTG	GAG	GTG	AAA	TAC	1506
Q	G	E	W	G	T	V	C	H	D	R	W	S	T	R	N	A	A	V	V	513
CAA	GGA	GAG	TGG	GGG	ACT	GTG	TGT	CAT	GAC	AGA	TGG	AGC	ACA	AGG	AAT	GCA	GCT	GTT	GTG	1566

Fig. 26C

C	K	Q	L	G	C	G	K	P	M	H	V	F	G	M	T	Y	F	K	E	533
TGT	AAA	CAA	TTG	GGA	TGT	GGA	AAG	CCT	ATG	CAT	GTG	TTT	GGT	ATG	ACC	TAT	TTT	AAA	GAA	1626
A	S	G	P	I	W	L	D	D	V	S	C	I	G	N	E	S	N	I	W	553
GCA	TCA	GGA	CCT	ATT	TGG	CTG	GAT	GAC	GTT	TCT	TGC	ATT	GGA	AAT	GAG	TCA	AAT	ATC	TGG	1686
D	C	E	H	S	G	W	G	K	H	N	C	V	H	R	E	D	V	I	V	573
GAC	TGT	GAA	CAC	AGT	GGA	TGG	GGA	AAG	CAT	AAT	TGT	GTA	CAC	AGA	GAG	GAT	GTG	ATT	GTA	1746
T	C	S	G	D	A	T	W	G	L	R	L	V	G	G	S	N	R	C	S	593
ACC	TGC	TCA	GGT	GAT	GCA	ACA	TGG	GGC	CTG	AGG	CTG	GTG	GGC	GGC	AGC	AAC	CGC	TGC	TCG	1806
G	R	L	E	V	Y	F	Q	G	R	W	G	T	V	C	D	D	G	W	N	613
GGA	AGA	CTG	GAG	GTG	TAC	TTT	CAA	GGA	CGG	TGG	GGC	ACA	GTG	TGT	GAT	GAC	GGC	TGG	AAC	1866
S	K	A	A	A	V	V	C	S	Q	L	D	C	P	S	S	I	I	G	M	633
AGT	AAA	GCT	GCA	GCT	GTG	GTG	TGT	AGC	CAG	CTG	GAC	TGC	CCA	TCT	TCT	ATC	ATT	GGC	ATG	1926
G	L	G	N	A	S	T	G	Y	G	K	I	W	L	D	D	V	S	C	D	653
GGT	CTG	GGA	AAC	GCT	TCT	ACA	GGA	TAT	GGA	AAA	ATT	TGG	CTC	GAT	GAT	GTT	TCC	TGT	GAT	1986
G	D	E	S	D	L	W	S	C	R	N	S	G	W	G	N	N	D	C	S	673
GGA	GAT	GAG	TCA	GAT	CTC	TGG	TCA	TGC	AGG	AAC	AGT	GGG	TGG	GGA	AAT	AAT	GAC	TGC	AGT	2046
H	S	E	D	V	G	V	I	C	S	D	A	S	D	M	E	L	R	L	V	693
CAC	AGT	GAA	GAT	GTT	GGA	GTG	ATC	TGT	TCT	GAT	GCA	TCG	GAT	ATG	GAG	CTG	AGG	CTT	GTG	2106

Fig. 26D

G	G	S	S	R	C	A	G	K	V	E	V	N	V	Q	G	A	V	G	I	713
GGT	GGA	AGC	AGC	AGG	TGT	GCT	GGA	AAA	GTT	GAG	GTG	AAT	GTC	CAG	GGT	GCC	GTG	GGA	ATT	2166
L	C	A	N	G	W	G	M	N	I	A	E	V	V	C	R	Q	L	E	C	733
CTG	TGT	GCT	AAT	GGC	TGG	GGA	ATG	AAC	ATT	GCT	GAA	GTT	GTT	TGC	AGG	CAA	CTT	GAA	TGT	2226
G	S	A	I	R	V	S	R	E	P	H	F	T	E	R	T	L	H	I	L	753
GGG	TCT	GCA	ATC	AGG	GTC	TCC	AGA	GAG	CCT	CAT	TTC	ACA	GAA	AGA	ACA	TTA	CAC	ATC	TTA	2286
M	S	N	S	G	C	T	G	G	E	A	S	L	W	D	C	I	R	W	E	773
ATG	TCG	AAT	TCT	GGC	TGC	ACT	GGA	GGG	GAA	GCC	TCT	CTC	TGG	GAT	TGT	ATA	CGA	TGG	GAG	2346
W	K	Q	T	A	C	H	L	N	M	E	A	S	L	I	C	S	A	H	R	793
TGG	AAA	CAG	ACT	GCG	TGT	CAT	TTA	AAT	ATG	GAA	GCA	AGT	TTG	ATC	TGC	TCA	GCC	CAC	AGG	2406
Q	P	R	L	V	G	A	D	M	P	C	S	G	R	V	E	V	K	H	A	813
CAG	CCC	AGG	CTG	GTT	GGA	GCT	GAT	ATG	CCC	TGC	TCT	GGA	CGT	GTT	GAA	GTG	AAA	CAT	GCA	2466
D	T	W	R	S	V	C	D	S	D	F	S	L	H	A	A	N	V	L	C	833
GAC	ACA	TGG	CGC	TCT	GTC	TGT	GAT	TCT	GAT	TTC	TCT	CTT	CAT	GCT	GCC	AAT	GTG	CTG	TGC	2526
R	E	L	N	C	G	D	A	I	S	L	S	V	G	D	H	F	G	K	G	853
AGA	GAA	TTA	AAT	TGT	GGA	GAT	GCC	ATA	TCT	CTT	TCT	GTG	GGA	GAT	CAC	TTT	GGA	AAA	GGG	2586
N	G	L	T	W	A	E	K	F	Q	C	E	G	S	E	T	H	L	A	L	873
AAT	GGT	CTA	ACT	TGG	GCC	GAA	AAG	TTC	CAG	TGT	GAA	GGG	AGT	GAA	ACT	CAC	CTT	GCA	TTA	2646

Fig. 26E

C	P	I	V	Q	H	P	E	D	T	C	I	H	S	R	E	V	G	V	893	
TGC	CCC	ATT	GTT	CAA	CAT	CCG	GAA	GAC	ACT	TGT	ATC	CAC	AGC	AGA	GAA	GTT	GGA	GTT	GTC	2706
C	S	R	Y	T	D	V	R	L	V	N	G	K	S	Q	C	D	G	Q	V	913
TGT	TCC	CGA	TAT	ACA	GAT	GTC	CGA	CTT	GTG	AAT	GGC	AAA	TCC	CAG	TGT	GAC	GGG	CAA	GTG	2766
E	I	N	V	L	G	H	W	G	S	L	C	D	T	H	W	D	P	E	D	933
GAG	ATC	AAC	GTG	CTT	GGA	CAC	TGG	GGC	TCA	CTG	TGT	GAC	ACC	CAC	TGG	GAC	CCA	GAA	GAT	2826
A	R	V	L	C	R	Q	L	S	C	G	T	A	L	S	T	T	G	G	K	953
GCC	CGT	GTT	CTA	TGC	AGA	CAG	CTC	AGC	TGT	GGG	ACT	GCT	CTC	TCA	ACC	ACA	GGA	GGA	AAA	2886
Y	I	G	E	R	S	V	R	V	W	G	H	R	F	H	C	L	G	N	E	973
TAT	ATT	GGA	GAA	AGA	AGT	GTT	CGT	GTG	TGG	GGA	CAC	AGG	TTT	CAT	TGC	TTA	GGG	AAT	GAG	2946
S	L	L	D	N	C	Q	M	T	V	L	G	A	P	P	C	I	H	G	N	993
TCA	CTT	CTG	GAT	AAC	TGT	CAA	ATG	ACA	GTT	CTT	GGA	GCA	CCT	CCC	TGT	ATC	CAT	GGA	AAT	3006
T	V	S	V	I	C	T	G	S	L	T	Q	P	L	F	P	C	L	A	N	1013
ACT	GTC	TCT	GTG	ATC	TGC	ACA	GGA	AGC	CTG	ACC	CAG	CCA	CTG	TTT	CCA	TGC	CTC	GCA	AAT	3066
V	S	D	P	Y	L	S	A	V	P	E	G	S	A	L	I	C	L	E	D	1033
GTA	TCT	GAC	CCA	TAT	TTG	TCT	GCA	GTT	CCA	GAG	GGC	AGT	GCT	TTG	ATC	TGC	TTA	GAG	GAC	3126
K	R	L	R	L	V	D	G	D	S	R	C	A	G	R	V	E	I	Y	H	1053
AAA	CGG	CTC	CGC	CTA	GTG	GAT	GGG	GAC	AGC	CGC	TGT	GCC	GGG	AGA	GTA	GAG	ATC	TAT	CAC	3186

Fig. 26F

D	G	F	W	G	T	I	C	D	D	G	W	D	L	S	D	A	H	V	V	1073
GAC	GGC	TTC	TGG	GGC	ACC	ATC	TGT	GAT	GAC	GGC	TGG	GAC	CTG	AGC	GAT	GCC	CAC	GTG	GTG	3246
C	Q	K	L	G	C	G	V	A	F	N	A	T	V	S	A	H	F	G	E	1093
TGT	CAA	AAG	CTG	GGC	TGT	GGA	GTG	GCC	TTC	AAT	GCC	ACG	GTC	TCT	GCT	CAC	TTT	GGG	GAG	3306
G	S	G	P	I	W	L	D	D	L	N	C	T	G	T	E	S	H	L	W	1113
GGG	TCA	GGG	CCC	ATC	TGG	CTG	GAT	GAC	CTG	AAC	TGC	ACA	GGA	ACG	GAG	TCC	CAC	TTG	TGG	3366
Q	C	P	S	R	G	W	G	Q	H	D	C	R	H	K	E	D	A	G	V	1133
CAG	TGC	CCT	TCC	CGC	GGC	TGG	GGG	CAG	CAC	GAC	TGC	AGG	CAC	AAG	GAG	GAC	GCA	GGG	GTC	3426
I	C	S	E	F	T	A	L	R	L	Y	S	E	T	E	T	E	S	C	A	1153
ATC	TGC	TCA	GAA	TTC	ACA	GCC	TTG	AGG	CTC	TAC	AGT	GAA	ACT	GAA	ACA	GAG	AGC	TGT	GCT	3486
G	R	L	E	V	F	Y	N	G	T	W	G	S	V	G	R	R	N	I	T	1173
GGG	AGA	TTG	GAA	GTC	TTC	TAT	AAC	GGG	ACC	TGG	GGC	AGC	GTC	GGC	AGG	AGG	AAC	ATC	ACC	3546
T	A	I	A	G	I	V	C	R	Q	L	G	C	G	E	N	G	V	V	S	1193
ACA	GCC	ATA	GCA	GGC	ATT	GTG	TGC	AGG	CAG	CAG	CTG	GGC	TGT	GGG	GAG	AAT	GGA	GTT	GTC	3606
L	A	P	L	S	K	T	G	S	G	F	M	W	V	D	D	I	Q	C	P	1213
CTC	GCC	CCT	TTA	TCT	AAG	ACA	GGC	TCT	GGT	TTC	ATG	TGG	GTG	GAT	GAC	ATT	CAG	TGT	CCT	3666
K	T	H	I	S	I	W	Q	C	L	S	A	P	W	E	R	R	I	S	S	1233
AAA	ACG	CAT	ATC	TCC	ATA	TGG	CAG	TGC	CTG	TCT	GCC	CCA	TGG	GAG	CGA	AGA	ATC	TCC	AGC	3726

Fig. 26G

P	A	E	E	T	W	I	T	C	E	D	R	I	R	V	R	G	G	D	T	1253
CCA	GCA	GAA	GAG	ACC	TGG	ATC	ACA	TGT	GAA	GAT	AGA	ATA	AGA	GTG	CGT	GGA	GGA	GAC	ACC	3786
E	C	S	G	R	V	E	I	W	H	A	G	S	W	G	T	V	C	D	D	1273
GAG	TGC	TCT	GGG	AGA	GTG	GAG	ATC	TGG	CAC	GCA	GGC	TCC	TGG	GGC	ACA	GTG	TGT	GAT	GAC	3846
S	W	D	L	A	E	A	E	V	V	C	Q	Q	L	G	C	G	S	A	L	1293
TCC	TGG	GAC	CTG	GCC	GAG	GCG	GAA	GTG	GTG	TGT	CAG	CAG	CTG	GGC	TGT	GGC	TCT	GCT	CTG	3906
A	A	L	R	D	A	S	F	G	Q	G	T	G	T	I	W	L	D	D	M	1313
GCT	GCC	CTG	AGG	GAC	GCT	TCG	TTT	GGC	CAG	GGA	ACT	GGA	ACC	ATC	TGG	TTG	GAT	GAC	ATG	3966
R	C	K	G	N	E	S	F	L	W	D	C	H	A	K	P	W	G	Q	S	1333
CGG	TGC	AAA	GGA	AAT	GAG	TCA	TTT	CTA	TGG	GAC	TGT	CAC	GCC	AAA	CCC	TGG	GGA	CAG	AGT	4026
D	C	G	H	K	E	D	A	G	V	R	C	S	G	Q	S	L	K	S	L	1353
GAC	TGT	GGA	CAC	AAG	GAA	GAT	GCT	GGC	GTG	AGG	TGC	TCT	GGA	CAG	TCG	CTG	AAA	TCA	CTG	4086
N	A	S	S	G	H	L	A	L	I	L	S	S	I	F	G	L	L	L	L	1373
AAT	GCC	TCC	TCA	GGT	CAT	TTA	GCA	CTT	ATT	TTA	TCC	AGT	ATC	TTT	GGG	CTC	CTT	CTC	CTG	4146
V	L	F	I	L	F	L	T	W	C	R	V	Q	K	Q	K	H	L	P	L	1393
GTT	CTG	TTT	ATT	CTA	TTT	CTC	ACG	TGG	TGC	CGA	GTT	CAG	AAA	CAA	AAA	CAT	CTG	CCC	CTC	4206
R	V	S	T	R	R	R	G	S	L	E	E	N	L	F	H	E	M	E	T	1413
AGA	GTT	TCA	ACC	AGA	AGG	AGG	GGT	TCT	CTC	GAG	GAG	AAT	TTA	TTC	CAT	GAG	ATG	GAG	ACC	4266

Fig. 26H

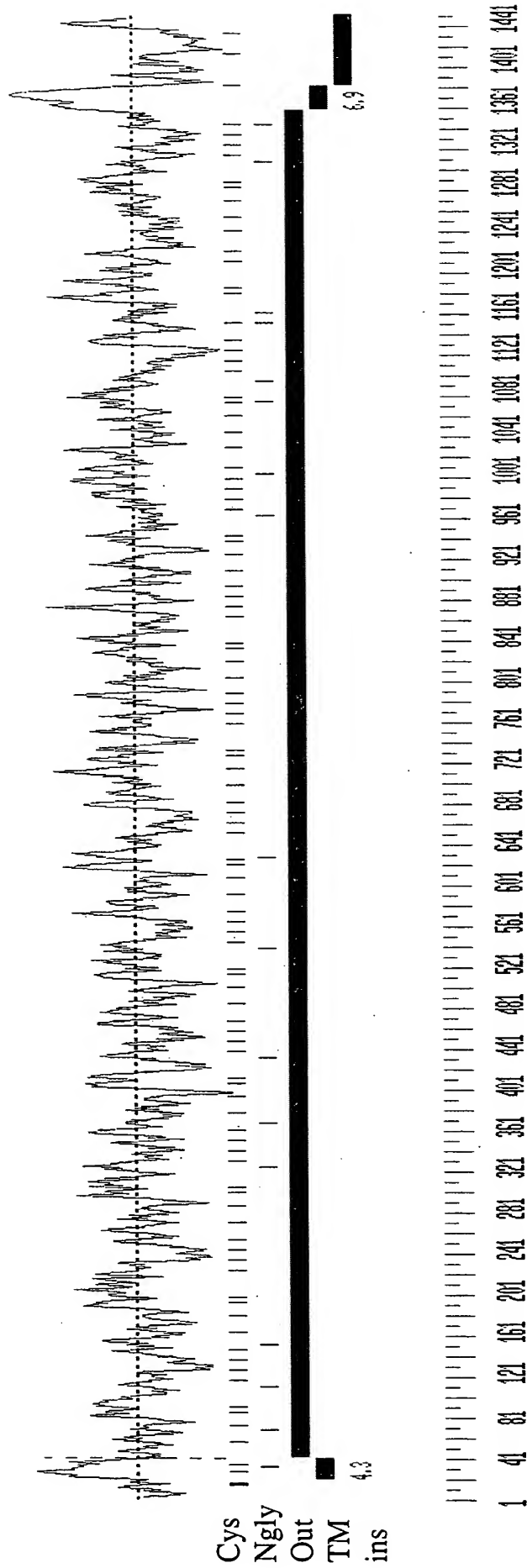


Fig. 26J

	10	20	30	40	50	60	70	
Hum.	MMLPQNSWHIDFGRCCCHQNLFSAVVTCILLNSCFLISSFNQTDLELRLVNGDGPCSGTVEVKFQGWG							
	:	:	:	:	:	:	:	
	:	:	:	:	:	:	:	
WC1	MAL-----GR---HLSLRGL---CVLLLLGT--MVG---GQALELRLKDGVHRCEGRVEVKHQGEWG	10	20	30	40	50		
	80	90	100	110	120	130		
Hum.	TVCDGWNNTASTVVCKQLGCPFSFAMFRFGQAVTR-HGKIWLDDVSCYGNESALWECQH--REWGSHN							
	:	:	:	:	:	:	:	
	:	:	:	:	:	:	:	
WC1	TVDGYRWTLKDASVVCRLGCGAAIG-FPGGAYFGPGLGPIWLLYTSCEGTESTVSDCEHSNIKDYRNDG	60	70	80	90	100	110	
	140	150	160	170	180	190	200	
Hum.	CYHGEDVGVNCYGEANLGLRLVDGNNSCSGRVEVKFQERWGTICDDGWNLTAAVVCRLGCPSSFSSG							
	:	:	:	:	:	:	:	
	:	:	:	:	:	:	:	
WC1	YNHGRDAGVVCSG----FVRLAGGDGPCSGRVEVHSGEAWIPVSDGNFTLATAQIICAELGCGKAVSVLG	120	130	140	150	160	170	180
	210	220	230	240	250	260	270	
Hum.	VNSPA VLRPIWLDDILCQGNELALWNCRHRGWGNHDCSHNEDVTLTICYDSSDLELRLVGGTNRCMGRVE							
	:	:	:	:	:	:	:	
	:	:	:	:	:	:	:	
WC1	HEL FRESSAQVWAEFRCEGEPELWVCPRPVCPGGTCHHSGSAQVVC SAYSEVRL-MTNGSSQCEGQVE	190	200	210	220	230	240	250

Fig. 26K

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280      290      300      310      320      330      340
Hum. LKIQGRWGTVCHHKWNNAADVCKQLGCGTALHFAGLPHLQSGSDVVWLDGVSCSGNESFLWDCRHS GT
    . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1 MNISQWRALCASHWISLANANVICRQLGCGVAISTPGPHLVEEGDQILTARFHCSGAESFLWSCPV TAL
260      270      280      290      300      310      320

350      360      370      380      390      400      410
Hum. VNFDC LHQNDVSVICSDGADLELRLADGSNNCSGRVEVRIHEQWWTICDQNWKNEQALVVC KQLGCPFSV
    . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1 GGPDCSHGNTASVICS-GNQI-----QVLPQCND-----SV
330      340      350

420      430      440      450      460      470      480
Hum. FGSRRAKPSNEARDIWINNISCTGNESALWDCTYDGKAKRTCRRSDAGVICSDKADLDRLVGAHSPCY
    . . . . . : : : : : : : : : : : : : : : : : : : : : : : : :
WC1 -----SQPTGSA-----ASEDSA----PY-----CSDSRQL--RLVDGGGPCA
360      370      380

490      500      510      520      530      540      550
Hum. GRLEVKYQGEWGTVCHDRWSTRNAAVVKQLGCGKPMHVFGMTYFKEASGPIWLDDVSCIGNESNIWDCE
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1 GRVEILDQGSWGTICDDGWDLD DARVVC RQLGCGEALNATGSAHFGAGSGPIWLDNLNCTGKESHVWRCP
390      400      410      420      430      440      450

```

Fig. 26L

	560	570	580	590	600	610	620	
Hum.	HSGWGKHNCHREDVIVTCSGDATWGLRLVGGSNRCSGRLEVFYFQGRWGTVCDDGWNKAAA VVCSQLDC							
	460	470	480	490	500	510	520	
WC1	SRGWQHNCRHKQDAGVICS--EFLALRMVSEDQQCAGWLEVFYNGTWGVCVRNPMEDITVSTICRQLGC							
	630	640	650	660	670	680	690	
Hum.	PSSIIGMGLGNASTGYGKIWLDDVSCDGEDSLWSCRNSGWNDCSHSEDVGVICSDASDMELRLVGG							
	530	540	550	560	570	580	590	
WC1	GDSGTLNSSVALREGFRPQWVDRIQCRKTDTSLWQCPSPDPWNYNSCSPKEEAYIWCADSR--QIRLVDGG							
	700	710	720	730	740	750	760	
Hum.	SRCAGKVEVNVQGA VGILCANGWGMNIAEVVCRQLECGSAIRVSREPHFTERTLHILMSNSGCTGGEASL							
	600	610	620	630	640	650	660	
WC1	GRCSGRVEILDQGSWG TICDDRWDLDDARVVC KQLGCGEALDATVSSFFGTGSGPIWLDEVNCRGEEESQV							
	770	780	790	800	810	820	830	
Hum.	WDCIRWEWKQTACHLNMEASLICS AHRQPRLVGADMP CSGRVEVKHADTWRSVCDSD FSLHAANVLCREL							
	670	680	690	700	710	720	730	
WC1	WRCPSWGWRQHNCNHQEDAGVICS GF--VRLAGDGP CSGRVEVHSGEAWTPVSDGNFTLPTAQVICAEL							

Fig. 26M

	840	850	860	870	880	890	900
Hum.	NCGDAISLSVGDHFGKGNGLTWAЕКFQCEGSETHLALCPIVQHPEDTCIHSREVGVCSRYTDVRLV-NG						
	:: ::::	:	:: ::::	:	:: ::::	:: ::::	:: ::::
WC1	GCGKAVSVLGHMPFRES	DGQVWAEER	CDGGEPELWSCPR	VP	PCPGGTCLHSGAAQV	CVSVTEVQLMKNG	
	740	750	760	770	780	790	800
	910	920	930	940	950	960	970
Hum.	KSQCDGQVEINVLGHWGSLCDTHWDPEDARVLCRQLSCGTALSTTGKYGIGERSVRVWGHFRHCLGNESL						
	:: ::::	:: ::::	:: ::::	:: ::::	:: ::::	:: ::::	:: ::::
WC1	TSQCEGQVEMKISGRWRALCASHWSLANANVVCRLGCGVAISTPRGPHLVEGGDQ	ISTAQFHCSGAESF					
	810	820	830	840	850	860	870
	980	990	1000	1010	1020	1030	1040
Hum.	LDNCQMTVLGAPPCIHGNTVSVICTGSLTQPLFPCLANVSDPYLSAVPEGSA						
	:	:: ::::	:: ::::	:	:: ::::	:	:: ::::
WC1	LWSCPVTALGGPDCSHGNTASVICSGNHTQVLPQCNDFLSQPAGSAASESSPYCSDSRQLRLVDGGGPC						
	880	890	900	910	920	930	940
	1050	1060	1070	1080	1090	1100	1110
Hum.	AGRVEIYHDFWGTICDDGWDLSDAHVVCQKLGCGVAFNATVSAHFGE						
	:: ::::	:: ::::	:: ::::	:: ::::	:: ::::	:: ::::	:: ::::
WC1	GGRVEILDQGSWGTICDDDDWDLD	DARVVCRLGCGEALNATGSAHF	GAGSGPIWLDDDLNCTKESHVWRC				
	950	960	970	980	990	1000	1010

Fig. 26N

	1120	1130	1140	1150	1160	1170	1180
Hum.	PSRGWQHDCRHKEDAGVICSEFTALRLYSETETESCAGRLEVFYNGTWGSVGRRNITTAIAGIVCRQLG						

WC1	PSRGWGRHDCRHKEDAGVICSEFLALRMVSEDQQ--CAGWLEVFYNGTWGSVCRSPMEDITVSVICRQLG						
	1020	1030	1040	1050	1060	1070	
	1190	1200	1210	1220	1230	1240	
Hum.	CGENGVS LAPLSKTGSGFMWVDIIQCPKTHISIWQCLSA PWERRISSPAEETWITCEDR-----						

WC1	CGDSGSLNTSVGLREGSRPRWVDLIQCRKMDTSLWQCPSPGWKYSSCSPKEEAYISCEGRRPKSCPTAAA						
	1080	1090	1100	1110	1120	1130	1140
	1250	1260	1270	1280	1290	1300	
Hum.	-----IRVRGGDTECSGRVEIWHAGSWGTVCDSDSLAEAEVVCQQLGCGSALALRDASFQGGGTGIW						

WC1	CTDREKLRLRGGDSECSGRVEVWHNGSWGTVCDSDSWSLAEAEVVCQQLGCGQALEAVRSAAFGPGNGSIW						
	1150	1160	1170	1180	1190	1200	1210
	1310	1320	1330	1340	1350	1360	
Hum.	LDDMRCKGNESFLWDCHAKPWGQSDCGHKEDAGVRCSG-----QSLKSLNASSGHLALI						

WC1	LDEVQCGGRESSLWDCVAEPWGQSDCKHEEDAGVRCSGVRTTLPTTAGTRTTSNSLPGIFSLPGVLC LI						
	1220	1230	1240	1250	1260	1270	1280

Fig. 260

Fig. 26P

Hum. ATGATGCTGCCTCAAAACCTCGTGGCATATTGATTTTGAAGATGCTGTGTCATCAGAACCTTTTCTCTCTG
 WC1 ATG-----GCTC-TGG-----GCAGACA-----CCTCT-CCCTG
 10 20

Fig. 26Q-1

```

280      290      300      310      320      330      340
Hum.  TCCTTCGCCAATGTTTCGTTTGGACAAGCCGTGA--CTAGACATGGAAAAAATTTGGCTTGATGATGTTTC
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
WC1   GCCATTG--GTTTCCCTGGAGGGGCTTATTTTGGCCAGGACTTGGCCCCCATTTGGCTTTTGATATACTTC
220    230    240    250    260    270    280
      350    360    370    380    390    400    410
Hum.  CTGTTATGGAAATGAGTCAGCTCTCTGGGAATGTCAACACCCGGAATGGGAAGCCATAACTGTTATCAT
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
WC1   ATGTGAAGGGACAGAGTCAACTGTCACTGAGTCACTGTGAGCAT-TCTAATATTAAGAC-TATC-GTAATGAT
290    300    310    320    330    340    350
      420    430    440    450    460    470    480
Hum.  GGAGAAGATGTTGGTGTGAACGTGTTATGGTGAAGCCAA-TCTGGGTTTGAG--GCTAG-TGGATGGAAAC
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
WC1   GGCATAATCATGTGTCGGGA--TGCTGGAGTAGTCTGCTCAGGATTTGTGCGTCTGGCTGGAGGGGATG
360    370    380    390    400    410    420
      490    500    510    520    530    540    550
Hum.  AACTCCTGTTCAGGGAGAGTGGAGGTGAAATTCCAAGAAAGGTGGGGGACTATATGTGATGATGGGTGGA
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
WC1   GAC-CCTGCTCAGGGCGAGTAGAAGTGCAATT--CTGGAGAAGCTTGGATCCCAGTGT-CTGATGGGAACT
430    440    450    460    470    480

```

Fig. 26Q-2

	560	570	580	590	600	610	620
Hum.	ACTTGAATACTGCTGCCGTGGTGTGCAGGCAACTAGGATGTCCATCTTCTTTTATTCTTCTGGAGTTGT						

WC1	TCACACTTGCCACTGCC-----CAG-----ATCATCTGT-----GCAGAGTTGGG						
	490	500		510		520	
	630	640	650	660	670	680	690
Hum.	TAATAGCCCTGCTGTATTGCGCCCCCATTTGGCTGGATGACATTTTATGCCAGGGAATGAGTTGGCACT-						

WC1	TTGTGGC-----AAGGCTG--TGCTCTGT-----CCTGGGACATGAG-----CTCTT						
	530		540		550	560	
	700	710	720	730	740	750	760
Hum.	CTGGAATTGCAGACATCGTGGATGGGAAATCATGACTGCAGTCACAATGAGGATGTCACATTAACTTGT						

WC1	CAGAGAGTCCAGT-GCC-----CAGGCTCG--GGC---TGAAGAGTTCA-----GG						
	570	580		590		600	
	770	780	790	800	810	820	830
Hum.	TATGATAGTAGTGATCTTGAACTAAGGCTTGTAGGTGGAACATAACCGCTGTATGGGGAGTAGAGCTGA						

WC1	TGTGAGGGGAGGAGCCTGAGCT---CT-----GGGTCTGCCC-CAGAGTG-----CCCTG-						
	610	620	630		640	650	

Fig. 26Q-3

	840	850	860	870	880	890	900
Hum.	AAATCCAAGGAAGTGGGGACCGTATGCCACCATAAGTGGAACAATGCTGCAGCTGATGTCGTATGCAA						
	:::	:::	:::	:::	:::	:::	:::
WC1	---TCCA-----GGGGCACGTGT--CACCACA-GTGGATC--TGCT-CAGGTTGTTTGTTCAGCAT						
	660	670	680	690	700		
	910	920	930	940	950	960	970
Hum.	GCAGTTGGGATGTGGAACCGCACCATTCACTTCGCTGGCTTGCCCTCATTTGCAGTCAGGGTCTGATGTTGTA						

WC1	ACT-----CAGAAGTCCGGCTCATGACAA-AC-GGCT--CCTC-TCAG-TGTGAAGGCGCAGGTGGAGAT						
	710	720	730	740	750	760	
	980	990	1000	1010	1020	1030	1040
Hum.	TGGCTTGATGGTGTCCTCGTCCGGTAATGAATCTTTCTTTGGACTGCAGACATTCCGGAACCGTCA						
	:
WC1	GAACATT-----TCTG-GACAAATGGAGAGCGCTCTGTGCCCTCCC-CTGGAGTCTGGCCCAATGCC---A						
	770	780	790	800	810	820	
	1050	1060	1070	1080	1090	1100	1110
Hum.	ATTTTGACTGTCTTCATCAAAACGATGTGTCTGTGATCTGCTCAGATGGAGCAGATTTGGAAC TCGGACT						
	::	::	::
WC1	ATGTTATCTGTCGTAGCTCGGCTGTGGAGTTGCCATCTCCACCCCGGAG-----GACCAC-ACT						
	830	840	850	860	870	880	

Fig. 26Q-4

Hum.	1120	1130	1140	1150	1160	1170	1180
	AGCAGATGGAAGTAACAATTTGTT	CAGGGAGAGTAGAGGTGAGAA	TTCA-TGAACAGTGGTGGACAATATG				
WC1	TG---GTGGAAGAAG---GTGATCAG--	ATCCTAACAGCCCGATTTCACTGCTCTG	-----GGGC-----TG				
	890	900	910	920	930		
Hum.	1190	1200	1210	1220	1230	1240	1250
	TGACCAGAACTGGAAGAAATGAACAAGCCCTTGTGGTTTGTAAAGCAGCTAGGATGTCCGTT	CAGCGTCTTT					
WC1	AGTCCT-TCCGTGGAGTTGT-----CCT-GTGACT-----GCC-CTGGGTGGTCCCTGACTGTTTCCCAT						
	940	950	960	970	980	990	
Hum.	1260	1270	1280	1290	1300	1310	1320
	GGCAG-TCGTCGTGCTAAACCTAGTAATGAAGCTAGAGACATTTGGATAAACAGCATATCTTGCAC	TGGG					
WC1	GGCAACACAGCCCTCTGTGATCTGCTCAGGAAACCAGATCCAGGTGCTTCCCCCAGTGCAACGA-CTCCG--						
	1000	1010	1020	1030	1040	1050	1060
Hum.	1330	1340	1350	1360	1370	1380	1390
	AATGAGTCAGCTCTCTGGGACTGCACATATGATGGAAAAGCAAGCGAACATGCTTCCGAAAGATCAGATG						
WC1	--TGTCCTCAACCTACAGGCTCTGC-----GGC-----CTCAGAGGACA-GCGCCC-----CCTACTG						
	1070	1080	1090	1100			

Fig. 26Q-5

	1400	1410	1420	1430	1440	1450	1460
Hum.	CTGGAGTAATT	TGTTCTGATAA	AGGCAGATCT	GGACCTAAG	GGCTTGTC	CGGGCTCAT	AGCCCCCTGTTATGG
	::	::	::	::	::	::	::
	::	::	::	::	::	::	::
WC1	CTCAGA-----	CAG--CAGGCAGCT	CCG--CCTGGTG---	GACGGGG-GC--	GGTCCCTGCGCCGG		
1110		1120	1130		1140	1150	1160
	1470	1480	1490	1500	1510	1520	
Hum.	GAGATTGGAGGT	GAAATACCAAG	GAGAGTGGGGG	ACTGTGTGTC	ATGACAGATG	GGAGCACAAGG-AA	TGC
	::	::	::	::	::	::	::
	::	::	::	::	::	::	::
WC1	GAGAGTGGAGAT	CCCTTGACCA	GGGCTCCTGGG	CACCATCTGT	GATGACGGCT	GGGAC-CTGG	ACGATGC
1170	1180	1190	1200	1210	1220		
	1530	1540	1550	1560	1570	1580	1590
Hum.	A-GCTGTTGTG	TGTAAACAATT	GGGATGTGGA-A	AGCCTATGC	ATGTGTTGGT	ATGACCTATTTTAAAG	
	::	::	::	::	::	::	::
	::	::	::	::	::	::	::
WC1	CCGC-GTGGTGT	GCAGGCAGCT	GGGCTGTGG	AGAAGCCCTCA-AT	GCCACGGGGT	CTGCTCACTTCGGGG	
1230	1240	1250	1260	1270	1280	1290	
	1600	1610	1620	1630	1640	1650	1660
Hum.	AAGCATCAGGAC	CTATT	TGGCTGGATG	ACGTTTCTT	GCATTGG	AAATGAGTCAAA	TATCTGGGACTGTGA
	::	::	::	::	::	::	::
	::	::	::	::	::	::	::
WC1	CAGGATCAGGG	CCCCATCT	GTGGTGACAACT	TGAAC	TGCACAGG	AAAGGAGTCCC	ACGTGTGGAGGTGCC
1300	1310	1320	1330	1340	1350	1360	

Fig. 26Q-6

	1950	1960	1970	1980	1990	2000	2010
Hum.	ATGTTTCCTGTGATGGAGATGAGTCAGATCTCTGGTCATGCAGGAACAGTGGTG--GGGAAATAATGAC						

WC1	-AGAAATCCAGTGTCTGGAAAACTGACACCTCTCT--CTGGCAGTGTCTTCTGACCCCTTGGAATTACAAC						
	1640	1650	1660	1670	1680	1690	1700
	2020	2030	2040	2050	2060	2070	2080
Hum.	TGCAGTCACAGTGAAGATGTTGGAGTG-ATCTGTTCTGATG-CATCGGATATGGAGCTGAGGCTTGTGGG						
	: : : :	: : : : .	: : : : .	: : : : .	: : : : .	: : : : .
WC1	T-CATGCTCTCCAAAGGAGGAAGCCCTATATCTGGTGTGCAGACAGCAGACA--GATCCGC--CTGGTGGA						
	1710	1720	1730	1740	1750	1760	
	2090	2100	2110	2120	2130	2140	2150
Hum.	TGGAAGCAGCAGGTGTGTGCTGGAAAGTTGAGGTGAATGTCCAGGGTGCCGTGGGAATTCTGTGTGCTAAT						
	: : : :	: : : : .	: : : : .	: : : : .
WC1	TGGAGGTGGTCGCTGCTCTGGGAGAGTGGAGATCCTTGACCAGGGCTCCTGGGGCACCATCTGTGATGAC						
	1770	1780	1790	1800	1810	1820	1830
	2160	2170	2180	2190	2200	2210	2220
Hum.	GGCTGGGGAATGAACATTGCTGAAGTTGTTTGCAGGCAACTTGAATGTGGGTCTGCAATCAGGGTCTCTCCA						

WC1	CGCTGGGACCTGGACGATGCCCGTGTGGTGTGCAAGCAGCTGGGCTGTGGAGAAGC---CCTGGACGCCA						
	1840	1850	1860	1870	1880	1890	1900

Fig. 26Q-8

	2230	2240	2250	2260	2270	2280
Hum.	GAGA-GCCTCATTTTCACAGAA--AGAACATTACACATCTTAATGTCGAATTC					
	1910	1920	1930	1940	1950	1960
WC1	CTGTCCTTCCCTTCTTCGGACGGGATCAGGGCCCATCTGGCTGGATGAAGTGA					
	2290	2300	2310	2320	2330	2340
Hum.	AGCCTCTCTCTGGGATTGTATACGATGGGAGTGGAACACAG-ACTGCGTGT					
	1980	1990	2000	2010	2020	2030
WC1	GTCCCAAGTATGGAGGTGCCCTTCCTGGGATGGCGCAACACAAAC-TGCAATCATCAAGAA					
	2360	2370	2380	2390	2400	2410
Hum.	TTTGATCTGCTCAGCCACAGGCAGCCAGGCTGGTTGGAGCTGATATGCCCTGCTCTGGACGTGTGAA					
	2050	2060	2070	2080	2090	2100
WC1	AGTCATCTGCTCAGGATTGTGC-----GTCTGGCTGGAGGAGATGGACCCCTGCTCAGGGCGAGTAGAA					
	2430	2440	2450	2460	2470	2480
Hum.	GTGAACATGCAGACACATGGCGCTCTGTCTGTGATTCCTGATTTCTCTCTTCA					
	2110	2120	2130	2140	2150	2160
WC1	GTGCATTCTGGAGAACCTGGACCCAGTGTCTGATGGAAACTTCACACTCCCCACTGCC					

Fig. 26Q-9

	2500	2510	2520	2530	2540	2550	2560
Hum.	GTGCAGAGAA	TTAAATTGTGGAGATGCCATATCTCTTTCTGTGGGAGATCACTTTGGAAAAGGG-AA	TGG				

WC1	GTGCAGAGC--TGGGATGTGGCAAGGCTGTGTCT-GTCCCTGGGACACATGCCATT	CAGAGATCCGATGG					
	2180	2190	2200	2210	2220	2230	2240
	2570	2580	2590	2600	2610	2620	2630
Hum.	TCTAACTTGGGCCGAAAAGTTCCAGTGTGAAGGGAGTGAAACTCACCTTG	CATTATGCCCCCATTTGTTCAA					

WC1	CCAGGTCTGGGCTGAAGAGTTCAGGTGTGATGGGGGGAGCCCTGAGCTCTGGT	CCTGCCCCAGAGTGCCC					
	2250	2260	2270	2280	2290	2300	2310
	2640	2650	2660	2670	2680	2690	2700
Hum.	CATCCGGAAGACACTTGTATCCACAGCAGAGAAAGTTGGAGTTGTCTGT	TCTCCGATATACAGATGTCCGAC					

WC1	TGTCCAGGAGGCACATGTCTCCACAGTGGAGCTGCTCAGGTTGTCTGT	TCAGTGTACACAGAAGTCCAGC					
	2320	2330	2340	2350	2360	2370	2380
	2710	2720	2730	2740	2750	2760	2770
Hum.	TTGTGAATGGCAAATCC--CAGTGTGACGGGCAAGTGGAGATCAACGTGCT-TGGACACTGGGGCTCAC						

WC1	TTATGAAAAACGGCACCTCTCAATGTGAGGGGCAGGTGGAGAT-GAAGATCTCT	TGGACGATGGAGAGCGC					
	2390	2400	2410	2420	2430	2440	2450

Fig. 26Q-10

	3060	3070	3080	3090	3100	3110	3120
Hum.	ATATTGCTGCAGTTCCAGAGGGCAGTGCTTTGATCTGCTTAGAGGACAAACGGCTCCGCCCTAGTGGAT						
	.	:::::.	:::::.	:::::.	:::::.	:::::.	:::::.
WC1	TGCAGGCTCTGCGGCCTCAGAGGAGAGTTCTCCCTACTGCTCAGACAGCAGGCTCCGCCCTGGTGGAC						
	2740	2750	2760	2770	2780	2790	2800
	3130	3140	3150	3160	3170	3180	3190
Hum.	GGGACAGCCGCTGTGCCGGGAGAGTAGAGATCTATCACGACGGCTTCTGGGGCACCATCTGTGATGACG						
	:::::.	:::::.	:::::.	:::::.	:::::.	:::::.	:::::.
WC1	GGGGCGGTCCCTGCGCGGGAGAGTGAGATCCTTGACCAAGGCTCCTGGGCACCATCTGTGATGATG						
	2810	2820	2830	2840	2850	2860	2870
	3200	3210	3220	3230	3240	3250	3260
Hum.	GCTGGACCTGAGCGATGCCCACGTGGTGTGTCAAAAGCTGGGCTGTGGAGTGGCCCTTCAATGCCACGGT						
	:::::.	:::::.	:::::.	:::::.	:::::.	:::::.	:::::.
WC1	ACTGGACCTGGACGATGCCCCGTGTGGTGTGCAGGCAGCTGGGCTGTGGAGAAAGCCCTCAATGCCACGGG						
	2880	2890	2900	2910	2920	2930	2940
	3270	3280	3290	3300	3310	3320	3330
Hum.	CTCTGCTCACTTTGGGAGGGGTCAGGGCCCATCTGGCTGGATGACCTGAACCTGCACAGGAACGGAGTCC						
	:::::.	:::::.	:::::.	:::::.	:::::.	:::::.	:::::.
WC1	GTCTGCTCACTTCGGGGCAGGATCAGGGCCCATCTGGCTGGACGACCTGAACCTGCACAGGAACGGAGTCC						
	2950	2960	2970	2980	2990	3000	3010

Fig. 26Q-12

Hum.	3340	3350	3360	3370	3380	3390	3400
	CAC	TGTGG	CAGTGCCCTTCCCGCGGCTGGGGCAGCACGACTGCAGGCACAAGGAGACGACGGGTCA				
	::: ::::	::: ::::	::: ::::	::: ::::	::: ::::	::: ::::	::: ::::
WC1	3020	3030	3040	3050	3060	3070	3080
	CACGTGTGGAGGTGCCCTTCCCGGGGCTGGGGCGGCACGACTGCAGACACAAGGAGACGCCGGGGTCA						
Hum.	3410	3420	3430	3440	3450	3460	3470
	TCTGCTCAGAAATTCACAGCCCTTGAGGCTCTACAGTGAAACTGAAACAGAGAGCTGTGCTGGAGATTGGA						
	::: ::::	::: ::::	::: ::::	::: ::::	::: ::::	::: ::::	::: ::::
WC1	3090	3100	3110	3120	3130	3140	
	TCTGCTCAGAGTTCCCTGGCCCTCAGGAT---GGTGAG-CGAGGACCAGCAG-TGTGCTGGGTGGCTGGA						
Hum.	3480	3490	3500	3510	3520	3530	3540
	AGTCTTCTATAACGGGACCTGGGGCAGCGTCGGCAGGAGGAACATCACACAGCCATAGCAGGCATTGTG						
	::: ::::	::: ::::	::: ::::	::: ::::	::: ::::	::: ::::	::: ::::
WC1	3150	3160	3170	3180	3190	3200	3210
	GGTTTCTACAACGGGACCTGGGGCAGTGCTGCCGAGCCCATGGAAGATATCACTGTGTCCGTGATC						
Hum.	3550	3560	3570	3580	3590	3600	
	TGCAGGCAGCTGGGCTGTGGGGAGAAATGGAGTTGTACGCCCTGCCCCCTTTA--TCT-AAGACAGGCTCTG						
	::: ::::	::: ::::	::: ::::	::: ::::	::: ::::	::: ::::	::: ::::
WC1	3220	3230	3240	3250	3260	3270	3280
	TGCAGACAGCTTGGATGTGGGGACAGTGGA--AGTCT-CAACACCTCTGTTGGTCTCAGGGAAGGTTCTA						

Fig. 26Q-13


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3840      3850      3860      3870      3880      3890      3900
Hum.  GGAAGTGGTGTCTCAGCAGCTGGGCTGTGGCTCTGCTCTGGCTGCCCTGAGGGACGCTTCGTTGGCCAG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1   TGAGGTGGTGTCTCAGCAGCTGGGCTGTGGCCAGGCCCTGGAAGCCGTGCGGCTCTGCAGCATTTGGCCCT
3570      3580      3590      3600      3610      3620      3630

3910      3920      3930      3940      3950      3960      3970
Hum.  GGAACCTGGAACCATCTGGTTGGATGACATGCGGTGCAAAAGGAAATGAGTCATTCTATGGGACTGTCACG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1   GGAAATGGGAGCATCTGGCTGGACGAGGTGCAGTGCAGGCGGGGCCGAGTCCTCCCTGTGGGACTGTGTTG
3640      3650      3660      3670      3680      3690      3700

3980      3990      4000      4010      4020      4030      4040
Hum.  CCAAACCCCTGGGGACAGAGTGACTGTGGACACAAAGGAAGATGCTGGCGTGAGGTGCTCTGG--ACAGTC
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1   CGGAGCCCTGGGGCAGAGCGACTGCAAGCACGAGGAGGATGCTGGTGTGAGGTGCTCTGGTGTAAAGGAC
3710      3720      3730      3740      3750      3760      3770

4050      4060      4070      4080      4090
Hum.  G-----CTGAAATCACTGAATG--CCT-----CCTCAGGT-CATT---TAGCA-CTTATTTTATCCA
      : . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1   AACATTGCCCCACGACCACAGCAGGGACCAGAACAACCTCAAATTCCTCCCTGGCATCTCTCCCTGCCT
3780      3790      3800      3810      3820      3830      3840

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Fig. 26Q-15

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4100      4110      4120      4130      4140
Hum. G-----TATCTT-----TGGGCTC-CTTCTC---CTGGTTCT-----GTTTATTCATTCTCA
      :      :      :      :      :      :      :      :      :      :
      :      :      :      :      :      :      :      :      :      :
WC1 GGGGTTCTCTGCCCTTATCCTGGGTCGCTTCTCTCCTGGTCCCTCGTCATCCTGGTGACTCAGCTACTCA
3850      3860      3870      3880      3890      3900      3910

4150      4160      4170      4180
Hum. CGTGGTG--CCGAGTTTCAGAAACAAAACATCT-----GCCC---CT-----CAGAGTTT-----
      :      :      :      :      :      :      :      :      :      :
      :      :      :      :      :      :      :      :      :      :
WC1 GATGGAGACAGAGCGCAGAGCCCTTATCCAGCTATGAAGATGCTCTTGGTGAAGCTGTGTATGAGGAGCT
3920      3930      3940      3950      3960      3970      3980

4190      4200      4210      4220
Hum. -----CAAC-----CAGAGGAGGG---GTTCT-CTCG---AGGAGAAATTATTCATGA-----
      :      :      :      :      :      :      :      :      :      :
      :      :      :      :      :      :      :      :      :      :
WC1 CGATTACCTTCTGACACAGAGGAAGTCTGGGCAGCCCAGATCAGATGACTGATGTCCCCTGATGAAAAT
3990      4000      4010      4020      4030      4040      4050

4230      4240      4250
Hum. ---GATGGAG-----ACCTG-----CCTC-----AAGAGAGAGGAC
      :      :      :      :      :      :      :      :      :      :
      :      :      :      :      :      :      :      :      :      :
WC1 TATGATGATGCTGAAGAAGTACCAGTGCCTGGAACCTCTCTCCCTCTCAGGGGAATGAGGAGGAAGTGC
4060      4070      4080      4090      4100      4110      4120

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Fig. 26Q-16

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4260      4270      4280      4290
Hum. CCACATGGGACAAAGAAC-----CTCAGA-TGACAC---CC-----CCAA-----
      :: :: :::: ::::: ::::: ::::: ::::: :::::
WC1  CCCAGAGAAAGGAGGACGGGTGAGGTCTCTCAGACAGGCTCTTCCCTGAACCTCTCCAGAGAGGCAGC
4130      4140      4150      4160      4170      4180      4190

      4300      4310      4320      4330
Hum. ----CCATGGTT--GTGAAGA----TGCTAGCGACAC-----ATCGCTG--TTGGGAGTT
      :: :: . ::::: : ::::: ::::: .. ::::: :::::
WC1  TAATCCCTGGGAAGGAGAGAGAGCTTCTGGCTGCTCCAGGGGAAGAAAGGGATGCTGGGTATGATGAT
4200      4210      4220      4230      4240      4250      4260

      4340      4350
Hum. CTT-----CCTG-----CCTCTGAAGCCACAAAA
      :: :::: ::::: ::::: ::::: :::::
WC1  GTTGAACTCAGTGCCCTGGGAACATCCCCAGTGACTTTCTCG
4270      4280      4290      4300

```

Fig. 26Q-17

GTCGACCCACGCGTCCGGTCTGTGGCTGAGC	M	A	L	P	A	L	G	L	D	P	W	S	12
	ATG	GCC	CTC	CCA	GCC	CTG	GGC	CTG	GAC	CCC	TGG	AGC	67
L L G L F L Q L L L L L P T T A G													32
CTC CTG GGC CTT TTC CTC TTC CAA CTG CTT CAG CTG CTG CTG CCG ACG ACG ACC GCG GGG													127
G G G Q G P M P R V R Y Y A G D E R A													52
GGA GGC GGC CAG GGC CCC ATG CCC AGG GTC AGA TAC TAT GCA GGG GAT GAA CGT AGG GCA													187
L S F F H Q K G L Q Q D F D T L L L S G D													72
CTT AGC TTC TTC CAC CAG AAG GGC CTC CAG GAT TTT GAC ACT CTG CTC CTG AGT GGT GAT													247
G N T L L Y V G A R E A I L A L D I Q D P													92
GGA AAT ACT CTC TAC GTG GGC GCT CGA GAA GCC ATT CTG GCC TTG GAT ATC CAG GAT CCA													307
G V P R L L K N M I P W P A S D R K K S E													112
GGG GTC CCC AGG CTA AAG AAC ATG ATA CCG TGG CCA GCC AGT GAC AGA AAA AAG AGT GAA													367
C A F K K K S N E T Q C F N F I R V L V													132
TGT GCC TTT AAG AAG AAG AGC AAT GAG ACA CAG TGT TTC AAC TTC ATC CGT GTC CTG GTT													427
S Y N V T H L Y T C G T F A F S P A C T													152
TCT TAC AAT GTC ACC CAT CTC TAC ACC TGC GGC ACC TTC GCC TTC AGC CCT GCT TGT ACC													487
F I E L L Q D S Y L L P I S E D K V M E G													172
TTC ATT GAA CTT CAA GAT TCC TAC CTG TTG CCC ATC TCG GAG GAC AAG GTC ATG GAG GGA													547

Fig. 27A

K	G	Q	S	P	F	D	P	A	H	K	H	T	A	V	L	V	D	G	M	192
AAA	GGC	CAA	AGC	CCC	TTT	GAC	CCC	GCT	CAC	AAG	CAT	ACG	GCT	GTC	TTG	GTG	GAT	GGG	ATG	607
L	Y	S	G	T	M	N	N	F	L	G	S	E	P	I	L	M	R	T	L	212
CTC	TAT	TCT	GGT	ACT	ATG	AAC	AAC	TTC	CTG	GGC	AGT	GAG	CCC	ATC	CTG	ATG	CGC	ACA	CTG	667
G	S	Q	P	V	L	K	T	D	N	F	L	R	W	L	H	H	D	A	S	232
GGA	TCC	CAG	CCT	GTC	CTC	AAG	ACC	GAC	AAC	TTC	CTC	CGC	TGG	CTG	CAT	CAT	GAC	GCC	TCC	727
F	V	A	A	I	P	S	T	Q	V	V	Y	F	F	F	E	E	T	A	S	252
TTT	GTG	GCA	GCC	ATC	CCT	TCG	ACC	CAG	GTC	GTC	TAC	TTC	TTC	TTC	GAG	GAG	ACA	GCC	AGC	787
E	F	D	F	F	E	R	L	H	T	S	R	V	A	R	V	C	K	N	D	272
GAG	TTT	GAC	TTC	TTT	GAG	AGG	CTC	CAC	ACA	TCG	CGG	GTG	GCT	AGA	GTC	TGC	AAG	AAT	GAC	847
V	G	G	E	K	L	L	Q	K	K	W	T	T	F	L	K	A	Q	L	L	292
GTG	GGC	GGC	GAA	AAG	CTG	CTG	CAG	AAG	AAG	TGG	ACC	ACC	TTC	CTG	AAG	GCC	CAG	CTG	CTC	907
C	T	Q	P	G	Q	L	P	F	N	V	I	R	H	A	V	L	L	P	A	312
TGC	ACC	CAG	CCG	GGG	CAG	CTG	CCC	TTC	AAC	GTC	ATC	CGC	CAC	GCG	GTC	CTG	CTC	CCC	GCC	967
D	S	P	T	A	P	H	I	Y	A	V	F	T	S	Q	W	Q	V	G	G	332
GAT	TCT	CCC	ACA	GCT	CCC	CAC	ATC	TAC	GCA	GTC	TTC	ACC	TCC	CAG	TGG	CAG	GTT	GGC	GGG	1027
T	R	S	S	A	V	C	A	F	S	L	L	D	I	E	R	V	F	K	G	352
ACC	AGG	AGC	TCT	GCG	GTT	TGT	GCC	TTC	TCT	CTC	TTG	GAC	ATT	GAA	CGT	GTC	TTT	AAG	GGG	1087

Fig. 27B

K	Y	K	E	L	N	K	E	T	S	R	W	T	T	Y	R	G	P	E	T	372
AAA	TAC	AAA	GAG	TTG	AAC	AAA	GAA	ACT	TCA	CGC	TGG	ACT	ACT	TAT	AGG	GGC	CCT	GAG	ACC	1147
N	P	R	P	G	S	C	S	V	G	P	S	S	D	K	A	L	T	F	M	392
AAC	CCC	CGG	CCA	GGC	AGT	TGC	TCA	GTG	GGC	CCC	TCC	TCT	GAT	AAG	GCC	CTG	ACC	TTC	ATG	1207
K	D	H	F	L	M	D	E	Q	V	V	G	T	P	L	L	V	K	S	G	412
AAG	GAC	CAT	TTC	CTG	ATG	GAT	GAG	CAA	GTG	GTG	GGG	ACG	CCC	CTG	CTG	GTG	AAA	TCT	GGC	1267
V	E	Y	T	R	L	A	V	E	T	A	Q	G	L	D	G	H	S	H	L	432
GTG	GAG	TAT	ACA	CGG	CTT	GCA	GTG	GAG	ACA	GCC	CAG	GGC	CTT	GAT	GGG	CAC	AGC	CAT	CTT	1327
V	M	Y	L	G	T	T	T	G	S	L	H	K	A	V	V	S	G	D	S	452
GTC	ATG	TAC	CTG	GGA	ACC	ACC	ACA	GGG	TCG	CTC	CAC	AAG	GCT	GTG	GTA	AGT	GGG	GAC	AGC	1387
S	A	H	L	V	E	E	I	Q	L	F	P	D	P	E	P	V	R	N	L	472
AGT	GCT	CAT	CTG	GTG	GAA	GAG	ATT	CAG	CTG	TTC	CCT	GAC	CCT	GAA	CCT	GTT	CGC	AAC	CTG	1447
Q	L	A	P	T	Q	G	A	V	F	V	G	F	S	G	G	V	W	R	V	492
CAG	CTG	GCC	CCC	ACC	CAG	GGT	GCA	GTG	TTT	GTA	GGC	TTC	TCA	GGA	GGT	GTC	TGG	AGG	GTG	1507
P	R	A	N	C	S	V	Y	E	S	C	V	D	C	V	L	A	R	D	P	512
CCC	CGA	GCC	AAC	TGT	AGT	GTC	TAT	GAG	AGC	TGT	GTG	GAC	TGT	GTC	CTT	GCC	CGG	GAC	CCC	1567
H	C	A	W	D	P	E	S	R	T	C	C	L	L	S	A	P	N	L	N	532
CAC	TGT	GCC	TGG	GAC	CCT	GAG	TCC	CGA	ACC	TGT	TGC	CTC	CTG	TCT	GCC	CCC	AAC	CTG	AAC	1627

Fig. 27C

S	W	K	Q	D	M	E	R	G	N	P	E	W	A	C	A	S	G	P	M	552
TCC	TGG	AAG	CAG	GAC	ATG	GAG	CGG	GGG	AAC	CCA	GAG	TGG	GCA	TGT	GCC	AGT	GGC	CCC	ATG	1687
S	R	S	L	R	P	Q	S	R	P	Q	I	I	K	E	V	L	A	V	P	572
AGC	AGG	AGC	CTT	CGG	CCT	CAG	AGC	CGC	CCG	CAA	ATC	ATT	AAA	GAA	GTC	CTG	GCT	GTC	CCC	1747
N	S	I	L	E	L	P	C	P	H	L	S	A	L	A	S	Y	Y	W	S	592
AAC	TCC	ATC	CTG	GAG	CTC	CCC	TGC	CCC	CAC	CTG	TCA	GCC	TTG	GCC	TCT	TAT	TAT	TGG	AGT	1807
H	G	P	A	A	V	P	E	A	S	S	T	V	Y	N	G	S	L	L	L	612
CAT	GGC	CCA	GCA	GCA	GTC	CCA	GAA	GCC	TCT	TCC	ACT	GTC	TAC	AAT	GGC	TCC	CTC	TTG	CTG	1867
I	V	Q	D	G	V	G	G	L	Y	Q	C	W	A	T	E	N	G	F	S	632
ATA	GTG	CAG	GAT	GGA	GTT	GGG	GGT	CTC	TAC	CAG	TGC	TGG	GCA	ACT	GAG	AAT	GGC	TTT	TCA	1927
Y	P	V	I	S	Y	W	V	D	S	Q	D	Q	T	L	A	L	D	P	E	652
TAC	CCT	GTG	ATC	TCC	TAC	TGG	GTG	GAC	AGC	CAG	GAC	CAG	ACC	CTG	GCC	CTG	GAT	CCT	GAA	1987
L	A	G	I	P	R	E	H	V	K	V	P	L	T	R	V	S	G	G	A	672
CTG	GCA	GGC	ATC	CCC	CGG	GAG	CAT	GTG	AAG	GTC	CCG	TTG	ACC	AGG	GTC	AGT	GGT	GGG	GCC	2047
A	L	A	A	Q	Q	S	Y	W	P	H	F	V	T	V	T	V	L	F	A	692
GCC	CTG	GCT	GCC	CAG	CAG	TCC	TAC	TGG	CCC	CAC	TTT	GTC	ACT	GTC	ACT	GTC	CTC	TTT	GCC	2107
L	V	L	S	G	A	L	I	I	L	V	A	S	P	L	R	A	L	R	A	712
TTA	GTG	CTT	TCA	GGA	GCC	CTC	ATC	ATC	CTC	GTG	GCC	TCC	CCA	TTG	AGA	GCA	CTC	CGG	GCT	2167

Fig. 27D

R	G	K	V	Q	G	C	E	T	L	R	P	G	E	K	A	P	L	S	R		732	
CGG	GGC	AAG	GTT	CAG	GGC	TGT	GAG	ACC	CTG	CGC	CCT	GGG	GAG	AAG	GCC	CCG	TTA	AGC	AGA		2227	
E	Q	H	L	Q	S	P	K	E	C	R	T	S	A	S	D	V	D	A	D		752	
GAG	CAA	CAC	CTC	CAG	TCT	CCC	AAG	GAA	TGC	AGG	ACC	TCT	GCC	AGT	GAT	GTG	GAC	GCT	GAC		2287	
N	N	C	L	G	T	E	V	A	*											762		
AAC	AAC	TGC	CTA	GGC	ACT	GAG	GTA	GCT	TAA											2317		
ACT	CTA	GGC	AC	AGG	CGG	CTG	CGG	TGC	AGG	CAC	CTG	GCC	CAT	GTG	CTG	GGC	GGC	CCCA	AGCAC	AGCCCTGACTAGGA	2396	
TGAC	AGC	AGC	ACAA	AAG	AC	CACTT	TCT	CCCC	TGAG	AGG	AGCTT	CTG	CTACT	CTG	CACTG	CACTG	ATG	ACACT	CAGCAGGG		2475	
TGAT	GCAC	AGC	AGT	CTGCC	CTCCCC	TAT	GGG	ACT	CCCC	TCT	TACCA	AGCAC	ATG	AGCT	CTCT	TAA	CAGG	TGGG	GCTACCC		2554	
CCAG	ACCT	GTCT	CCTAC	ACTG	ATATT	GAAGA	ACCT	GGAG	AGAT	CCCT	CAGT	TTCT	GGCC	AT	TCC	AGG	ACC	CTCC	CAGAAA		2633	
CAC	AGT	TTCA	AGAG	ATCCT	AAAA	AAAC	CTGCC	TGT	CCC	AGG	ACCC	TAT	GGT	AAT	GAAC	ACCA	CAATCT	AAACA	ATC		2712	
ATAT	GCTA	ACAT	GCC	ACT	CTGG	AAACT	CCACT	CTGA	AGCT	GCC	CGCT	TTG	GAC	ACCA	CACT	CCCC	TCT	CCCC	AGGGTCA		2791	
TGC	AGG	ATCT	GT	CCCC	CT	CTG	CTT	ACCA	GT	CGT	GAC	CCG	CTG	ACT	CCC	AGGA	GTCT	TTCT	GAA	GTCTGACC	2870	
ACCT	TTCT	TTCT	TTG	CTT	CA	GT	TGGG	CAG	ACT	CTG	AT	CCCT	CT	GC	CCCT	GGC	AGAA	TGGC	AGGGTAA	CTGAGCC	TTCT	2949
TCAC	TCCT	TTAC	CCCT	AG	CCCT	TC	ACCT	CT	CCCC	CT	CCCC	TTT	CCCT	TTT	GGG	AT	TCAG	AAAA	AACT	GCTTGTC		3028
AGAG	ACT	GTTT	ATTT	TTT	AT	TA	AAAT	ATA	AGG	CTT	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AGGCGGCCGC		3104

Fig. 27E

Hum.	10	20	30	40	50	60	70
	MALPALGLDPWSLLGLFLFQLQLLLPTTTAGGGGQGPMPRVRYAGDERRALSFFHQKGLQDFDTLLLS						

Mur.	10	20	30	40	50	60	70
	MALPSLGQDSWSLLRVFFQLFLPSLPPASGTGGQGPMPRVKYHAGDGHRALESFFQOKGLRDFDTLLLS						

Hum.	80	90	100	110	120	130	140
	GDGNTLYVGAREAILALDIQDPGVPRLKNMIPWPASDRKKSECAFKKSNETQCFNFIIRLVSYNVTHLY						

Mur.	80	90	100	110	120	130	140
	DDGNTLYVGARETVLALNIQNPGIPRLKNMIPWPASERKKTECAFKKSNETQCFNFIIRLVSYNATHLY						

Hum.	150	160	170	180	190	200	210
	TCGTFAFSPACTFIELQDSYLLPISEDKVMEKGQSPFDPAHKHTAVLVDGMLYSGTMNFLGSEPILMR						

Mur.	150	160	170	180	190	200	210
	ACGTFAFSPACTFIELQDSLLLPILIDKVMGKGQSPLTFTSTQAVLVDGMLYSGTMNFLGSEPILMR						

Hum.	220	230	240	250	260	270	280
	TLGSQPVLTDFLRWLHHDASFVAaipSTQVVVFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQ						

Mur.	220	230	240	250	260	270	280
	TLGSHPVLTDFLRWLHHDASFVAaipSTQVVVFFFEETASEFDFFEEELYISRVAQVCKNDVGGEKLLQ						

Fig. 27F

	290	300	310	320	330	340	350
Hum.	KKWTTFLKAQLLCTOPGQLPFNVIRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVF						

Mur.	KKWTTFLKAQLLCAQPGQLPFNIIRHAVLLPADSPSVSRIYAVFTSQWQVGGTRSSAVCAFSLLDIERVF						
	290	300	310	320	330	340	350
	360	370	380	390	400	410	420
Hum.	KGKYKELNKETSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFMLMDEQVVGTPLLVKSGVEYTRLAV						

Mur.	KGKYKELNKETSRWTTYRGSEVSPRPGSCSMGPSSDKALTFMKDHFMLMDEHVVGTPLLVKSGVEYTRLAV						
	360	370	380	390	400	410	420
	430	440	450	460	470	480	490
Hum.	ETAQGLDGHSHLVMYLGTGTLHKAVVSGDSSAHLVEEIQLPDPEPVRNLQLAPTQGA VFGFSGGVW						

Mur.	ESARGLDGSSHVMYLGTSTGPLHKAVVPQDSSAYLVEEIQLPDSEPVRLQLAPAQGA VFAFGSGGIW						
	430	440	450	460	470	480	490
	500	510	520	530	540	550	560
Hum.	RVPRANC SVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNSWKQDMERGNPEWACASGPMRSRLRPQS						

Mur.	RVPRANC SVYESCVDCVLARDPHCAWDPESTRCLLSGST-KPWKQDMERGNPEWVCTRGPMA RSPRRQS						
	500	510	520	530	540	550	

Fig. 27G

	570	580	590	600	610	620	630
Hum.	RPQIIKEVLAVPNSILELPCPHLSALASYWWSHGPAAVPEASSTVYNGSLLLIVQDGVGGLYQCWATENG						

Mur.	PPQLIKEVLTVPNSILELRCPHLSALASYWWSHGGRAKISEASATVYNGSLLLIPQDGVGGLYQCVATENG						
	560	570	580	590	600	610	620
	640	650	660	670	680	690	700
Hum.	FSYPVISYWVDSQDQTLALDPELAGIPREHVKVPLTRVSGGAALAAQQSYWPHFVTVTLFALVLSGALI						

Mur.	YSYPVVSYWVDSQDQPLALDPELAGVPREVRVQVPLTRVGGASMAAQRSYWPHFLIVTVLLAIVLLGLVLT						
	630	640	650	660	670	680	690
	710	720	730	740	750	760	
Hum.	ILVASPLRALRARGKVQGCETLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA						

Mur.	LLLASPLGALRARGKVQCGMLPPREKAPLSRDQHLQPSKDHRTSASDVDADNNHLGAEVA						
	700	710	720	730	740	750	760

Fig. 27H

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Hum.  GTCG-AC-CC-----ACG-----CGTCCGGT-----CTGTGGCTGAGCATGGC
      :: :: ::
Mur.  CTCGGACGCCCTGGGTTAGGGTCTGTACTGCTGGGGAACCATCTGGTGACCATCTCAGGCTGACCATGGC
      10 20 30 40 50 60 70
      40 50 60 70 80 90 100
Hum.  CCTCCCAGCCCTGGGCCCTGGACCCCTGGAGCCCTCTGGGCCCTTTCCCTCTTCCAACCTGCTTC-AGCTGCT
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Mur.  CCTACCATCCCTGGGCCAGGACTCATGGAGTCTCCTGCGTGTTTTTTCTTCCAACT-CTTCCTGCTGCC
      80 90 100 110 120 130
      110 120 130 140 150 160 170
Hum.  GCTGCCGACGACACCGCGGGGGAGGCGGGCAGGGGCCCATGCCAGGTCAGATACTATGCAGGGGAT
      . :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Mur.  ATCACTGCCACCTGCTTCTGGGACTGGTGGTCAGGGGCCCATGCCCCAGAGTCAAATACCATGCTGGAGAC
      140 150 160 170 180 190 200
      180 190 200 210 220 230 240
Hum.  GAACGTAGGGCACTTAGCTTCTTCCACCAGAAAGGCCCTCCAGGATTTTGACACTCTGCTCCTGAGTGGTG
      :... :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Mur.  GGGCACAGGGCCCTCAGCTTCTTCCAAACAAAGGCCCTCCGAGACTTTGACACGCTGCTCCTGAGTGACG
      210 220 230 240 250 260 270

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Fig. 27I

250	260	270	280	290	300	310	
Hum.	ATGGAATACTCT	ACGTGGGGCT	CGAGAGCCAT	TCTGGCCTT	GGATATCCAG	GATCCAGGGT	CCCC
	::: ::	::: ::	::: ::	::: ::	::: ::	::: ::	::: ::
Mur.	ATGGCAACACT	CTCTATGTGG	GGCTCGAGAG	ACCGTCCTGG	CCTTGAATAT	CCAGAACCCAG	GAATCCC
280	290	300	310	320	330	340	
Hum.	CAGGCTAAAGA	ACATGATAC	CGTGCCAGCC	AGTGACAGAAA	AAGAGTGATG	TGCCTTTAA	GAAAGAAG
	::: ::	::: ::	::: ::	::: ::	::: ::	::: ::	::: ::
Mur.	AAGGCTAAAGA	ACATGATAC	CGTGCCAGCC	AGTGAGAGAAA	AAGACCCGAAT	GTGCCTTTAA	GAAAGAAG
350	360	370	380	390	400	410	
Hum.	AGCAATGAGAC	ACAGTGTTT	CAACTTCAT	CCGTGTCCTGG	TTCTTACAAT	GTCAACC	ATCTCTACACCT
	::: ::	::: ::	::: ::	::: ::	::: ::	::: ::	::: ::
Mur.	AGCAATGAGAC	ACAGTGTTT	CAACTTCAT	TCGAGTCCTGG	TCTCTTACAAT	GTCTACCTC	ATATGCCT
420	430	440	450	460	470	480	
Hum.	460	470	480	490	500	510	520
	GCGGCACCTT	CGCCCTTC	AGCCCTG	CTTGTA	CCCTTCAT	TGAACTT	CAAGATTCC
	::: ::	::: ::	::: ::	::: ::	::: ::	::: ::	::: ::
Mur.	GTGGGACCTT	TGCCCTTC	AGCCCTG	CGCTGTA	CCCTTCAT	TGAACTT	CAAGATTCC
490	500	510	520	530	540	550	
	CTTGTGCC	CATCTT	CGCCAT	CTT	CGCCAT	CTT	CGCCAT

Fig. 27J

Hum.	GGAGGACAAAGGTCATGGAGGGAAGCCCAAGCCCTTTGACCCCGCTCACAAGCATACG-GCTGTCTTT	530	540	550	560	570	580	590
Mur.	GATAGACAAAGGTCATGGACGGGAAGGCCAAAGCCC-TTTGACCCCTGTTCAAGCACACAAAGCTGTCTTT	560	570	580	590	600	610	620
Hum.	GGTGGATGGGATGCTCTATTCTGGTACTATGAACAACCTTCCCTGGCAGTGAGCCCATCCTGATGCGCACACA	600	610	620	630	640	650	660
Mur.	GGTCGATGGGATGCTTTATTCCGGCACCATGAACAACCTTCCCTGGCAGCGAGCCCATCCTGATGCGGACACA	630	640	650	660	670	680	690
Hum.	CTGGGATCCCAGCCTGTCTCCTCAAGACCGACAACCTTCCCTCCGCTGGCTGCATCATGACGCCCTCCTTTGTGG	670	680	690	700	710	720	730
Mur.	CTGGGATCCCATCCTGTCTCTCAAGACTGACATCTTCTTACGCTGGCTGCACGCGGATGCCCTCCTTCGTGG	700	710	720	730	740	750	760
Hum.	CAGCCATCCCCTTCGACCCAGGTCGTCCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGA	740	750	760	770	780	790	800
Mur.	CAGCCATTCATCCACCCAGGTCGTCCTATTCTTCTTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGA	770	780	790	800	810	820	830

Fig. 27K

	810	820	830	840	850	860	870
Hum.	GAGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAGAAATGACGTGGCGGGCGGAAAAGCTGCTGCAGAAG						
	: : :
Mur.	AGAGCTGTATATATCCAGGGTGGCTCAAGTCTGCAAGAACGACGTGGCGGTGAAAAGCTGCTGCAGAAG						
	840	850	860	870	880	890	900
	880	890	900	910	920	930	940
Hum.	AAGTGGACCACCTTCCTGAAGCCCAGCTGCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCC						

Mur.	AAGTGGACCACCTTCCTCAAAGCCCAGTTGCTCTGCGCTCAGCCAGGGCAGCTGCCATTCAACATCATCC						
	910	920	930	940	950	960	970
	950	960	970	980	990	1000	1010
Hum.	GCCACGGGTCCTGCTCCCCGCCGATTCTCCACAGCTCCCCACATCTACGCAGTCTTCACTCCAGTG						

Mur.	GCCACGGGTCCTGCTGCCCGCCGATTCTCCCTCTGTGTTCCCGCATCTACGCAGTCTTTACCTCCAGTG						
	980	990	1000	1010	1020	1030	1040
	1020	1030	1040	1050	1060	1070	1080
Hum.	GCAGGTTGGCGGACCAGGAGCTCTGCGGTTTGTGCCCTTCTCTCTCTTGACATTGAACGTGCTTTAAG						

Mur.	GCAGGTTGGCGGACCAGGAGCTCAGCAGTCTGTGCCCTTCTCTCTCAGGACATTGAGCGAGTCTTTAA						
	1050	1060	1070	1080	1090	1100	1110

Fig. 27L

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1090      1100      1110      1120      1130      1140      1150
Hum.  GGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAACCCCC
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Mur.  GGGAGTACAAAGGAGCTGAACAAGGAGACCTCCCGCTGGACCACTTACCGGGGCTCAGAGGTCAGCCCCGA
1120      1130      1140      1150      1160      1170      1180

1160      1170      1180      1190      1200      1210      1220
Hum.  GGCCAGGCAGTTGCTCAGTGGGCCCTCCTCTGTGATAAGGCCCTGACCTTCATGAAGACCATTTCCTGAT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Mur.  GGCCAGGCAGTTGCTCCATGGGCCCTCCTCTGTGACAAAGCCCTTGACCTTCATGAAGACCATTTCCTGAT
1190      1200      1210      1220      1230      1240      1250

1230      1240      1250      1260      1270      1280      1290
Hum.  GGATGAGCAAGTGGTGGGACGCCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Mur.  GGATGAGCACGTGGTAGGAACACCCCTGCTGGTGAAGTCTGGTGTGGAGTACACACGGCTTGCTGTGGAG
1260      1270      1280      1290      1300      1310      1320

1300      1310      1320      1330      1340      1350      1360
Hum.  ACAGCCCAGGGCCTTGATGGGCACAGCCCATCTTGTCATGTACCTGGGAACCAACACAGGTCGCTCCACA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Mur.  TCAGCTCGGGGCCTTGATGGGAGCAGCCATGTGGTCATGTATCTGGGTACCTCCACGGGTCCCCTGCACA
1330      1340      1350      1360      1370      1380      1390

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Fig. 27M

	1370	1380	1390	1400	1410	1420	1430
Hum.	AGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAGAGATTTCAGCTGTTCCCTGACCCCTGAACC						
	::::::::::::	:	::::::::::::	::::	::::::::::::	::::	::::::::::::
Mur.	AGGCTGTGGTGCCCTCAGGACAGCAGTGCTTATCTCGTGGAGGAGATTTCAGCTGAGCCCTGACTCTGAGCC						
	1400	1410	1420	1430	1440	1450	1460
	1440	1450	1460	1470	1480	1490	1500
Hum.	TGTTCGCAACCTGCAGCTGGCCCCACCCAGGGTGCAGTGTTGTAGGCTTCTCAGGAGGTGTCTGGAGG						
	:::::	::::::::::::	::::::::::::	::::::::::::	::::::::::::	::::::::::::	::::::::::::
Mur.	TGTTCGAAACCTGCAGCTGGCCCCCGCCCCAGGGTGCAGTGTTGCAGGCTTCTCTGGAGGCATCTGGAGA						
	1470	1480	1490	1500	1510	1520	1530
	1510	1520	1530	1540	1550	1560	1570
Hum.	GTGCCCCGAGCCAACCTGTAAGTGTCTATGAGAGCTGTGTGGACTGTGTCCCTTGCCCGGACCCCACTGTG						
	::	::	::::::::::::	::::::::::::	::::::::::::	::::::::::::	::::::::::::
Mur.	GTTCCCAAGGGCCAATTGCAGTGTCTACGAGAGCTGTGTGGACTGTGTGCTTGCCAGGGACCCCTCACTGTG						
	1540	1550	1560	1570	1580	1590	1600
	1580	1590	1600	1610	1620	1630	1640
Hum.	CCTGGGACCCCTGAGTCCCGAACCTGTTGCCCTCCTGTCTGCCCCCAACCTGAACCTCCTGGAAGCAGGACAT						
	::::::::::::	::::::::::::	::	::::	::::::::::::	:	::::::::::::
Mur.	CCTGGGACCCCTGAATCAAGACTCTGCAGCCTTCTGTCTGGCTC-TACCAAGCCT--TGGAAGCAGGACAT						
	1610	1620	1630	1640	1650	1660	1670

Fig. 27N

	1650	1660	1670	1680	1690	1700	1710
Hum.	GGAGCGGGGA	ACCCAGAGTGGGCATGTGCCAGTGGCCCCCATGAGCAGGAGCCCTTCGGCCCTCAGAGCCGC					
	::: ::	::: ::	::: ::	::: ::	::: ::	::: ::	::: ::
Mur.	GGAACGCGGA	ACCCGGAGTGGGTATGCACCCGTGGCCCCCATGGCCAGGAGCCCCCGCGTCAAGAGCCCC					
	1680	1690	1700	1710	1720	1730	1740
	1720	1730	1740	1750	1760	1770	1780
Hum.	CCGCAATCAT	TAAAGATCCTGGCTGTCCCAACTCCATCCTGGAGCTCCCCCTGCCCCACCTGTCTAG					
	:: ::	::: ::	::: ::	::: ::	::: ::	::: ::	::: ::
Mur.	CCTCAACTAA	TAAAGAAGTCTGACAGTCCCAACTCCATCCTGGAGCTGGCTGCCCCACCTGTCTAG					
	1750	1760	1770	1780	1790	1800	1810
	1790	1800	1810	1820	1830	1840	1850
Hum.	CCTTGGCCCT	TATTATTTGGAGTCATGGCCAGCAGCAGTCCAGAGCCCTCTTCCACTGTCTACAATGG					
	:	::: ::	::: ::	::: ::	::: ::	::: ::	::: ::
Mur.	CACTGGCCCT	TTACCACTGGAGTCATGGCCGAGCCAAAATCTCAGAAAGCCTCTGTACCGTCTACAATGG					
	1820	1830	1840	1850	1860	1870	1880
	1860	1870	1880	1890	1900	1910	1920
Hum.	CTCCCTCTTG	CTGATAGTGCAGGATGGAGTTGGGGTCTCTACCAGTGTGGCAACTGAGAAATGGCTTT					
	::: ::	::: ::	::: ::	::: ::	::: ::	::: ::	::: ::
Mur.	CTCCCTCTTG	CTGCTGCCGAGGATGGTGTCTGGGGCCCTCTACCAGTGTGTGGCGACTGAGAACGGCTAC					
	1890	1900	1910	1920	1930	1940	1950

Fig. 270

	1930	1940	1950	1960	1970	1980	1990
Hum.	TCATACCCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGACCCCTGGCCCTGGATCCTGAAC	TTGGCAG					
	::::::::::::::::	::::::::::::::::	::::::::::::::::	::::::::::::::::	::::::::::::::::	::::::::::::::::	::::::::::::::::
Mur.	TCATACCCCTGTGGTCTCCTATTGGGTAGACAGCCAGGACCAGCCCTGGCGCTGGACCCCTGAGCTGGCGG						
	1960	1970	1980	1990	2000	2010	2020
	2000	2010	2020	2030	2040	2050	2060
Hum.	GCATCCCCCGGAGCATGTGAAGTCCCGTTGACCAAGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCA						
	:::	:::	:::	:::	:::	:::	:::
Mur.	GCGTTCCCCCGTGAGCGTGTGCAGGTCCCGCTGACCAAGGTCGGAGCGGAGCTTCCATGGCTGCCCAGCG						
	2030	2040	2050	2060	2070	2080	2090
	2070	2080	2090	2100	2110	2120	2130
Hum.	GTCCCTACTGGCCCCACTTTGTCACTGTCACTGTCCCTCTTGGCCTTAGTGCTTTCAGGAGCCCTCATCATC						
	::::::::::::::::	::::::::	::::::::	::::::::	::::::::	::::::::	::::::::
Mur.	GTCCCTACTGGCCCCCATTTTCTCATCGTTACCGTCCCTCGGCCATCGTGCTCCTGGGAGTGCTCACTCTC						
	2100	2110	2120	2130	2140	2150	2160
	2140	2150	2160	2170	2180	2190	2200
Hum.	CTCGTGGCCCTCCCCATTGAGAGCACTCCGGGCTCGGGCAAGGTTACGGGCTGTGAGACCCCTGCGCCCTG						
	:::	:::	:::	:::	:::	:::	:::
Mur.	CTCCTCGCTTCCCCACTGGGGGCGCTGCGGGCTCGGGGTAAGTTACGGGCTGTGGGATGCTGCCCCCCCA						
	2170	2180	2190	2200	2210	2220	2230

Fig. 27P

Hum.	GGGAGAGGCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGA	2210	2220	2230	2240	2250	2260	2270
Mur.	GGGAAAAGGCTCCACTGAGCAGGAGCACCTCCAGCCCTCCAAGACCAACAGGACCTCTGCCAGTGA	2240	2250	2260	2270	2280	2290	2300
Hum.	TGTGGACGCTGACAACAACCTGCCCTAGGCACCTGAGGTAGCTTAACTCTAGGCACAGG-CCGGGGCTG--C	2280	2290	2300	2310	2320	2330	2340
Mur.	CGTAGATGCCGACAAACAACCATCTGGGGCGCCGAAGTGGCTTAAACA-GGGACACAGATCCGCAGCTGAGC	2310	2320	2330	2340	2350	2360	2370
Hum.	GGTGACGGCACCTGGCCATGCTGGCTGGCGGCCCAAGCACAGCCCTGACTAGGATGACAGCAGCACAAA	2350	2360	2370	2380	2390	2400	2410
Mur.	AGAGCAAGCCACTGGCCCTGTTGGCTATGC---CAGGCACAG-----TGCCACTCT--	2380	2390	2400	2410	2420		
Hum.	AGACCACCTTTCTCCCCCTGAGAGGAGCTTCTGTACTCTGCATCACTGATGACACTCAGCAGGGTGATGC	2420	2430	2440	2450	2460	2470	2480
Mur.	-GACCA-----GGGTAGGAG--GCT-CT-C-CTGCTA-ACGTGTGTCACTACAG-----C	2430	2440	2450	2460	2470	2480	

Fig. 27Q

	2490	2500	2510	2520	2530	2540	2550
Hum.	ACAGCAGTCTG-CCTCCCCATGGGACTCCCTTTACC AAGCACATGAGCTCTCTAACAGGGTGGGGCT						
	:: :::: : :::::::::::::::::::: :::::::::::						::::::
Mur.	ACC-CAGTAGGTCCCTCCCCTGTGGGACTCTCTTC TGC-AAGCACATT-----GGGCT						
	2470	2480	2490	2500	2510		
	2560	2570	2580	2590	2600	2610	
Hum.	ACCCCCAGACCTGCTCCTACACTGATA-TTGAAGA AACCTGGAGAGGATCCTTCAGTTCTGGCCA TTCCAG						
	. : :::: :::: : . ::::: . :::::::::::::: ::::: ::::: ::::: .. ::::						
Mur.	GTCGCCATACCTGTACTTGTCGTGTGACAGGAAGAGCCAGAC-AGGTTTCTTTTGATTTTGATTGACCCAA						
	2520	2530	2540	2550	2560	2570	2580
	2620	2630	2640	2650	2660	2670	2680
Hum.	GGACCCCT-CCAGAAAACACA-GTGTTTCAAGAGATCCTA AAAAACCTGCCCTGTCCCAGGACCC TATGGTA						
	: ::::: ::::::::::: : ::::: :::::::::::::: ::::: ::::: ::::: :::::::::::						
Mur.	GAGCCCTGCCCTGTAAACAAACGTGCTCCAGGAGA-CCATGAAAGGTGTGGCTGTCT-GGGATTCTGTGGTG						
	2590	2600	2610	2620	2630	2640	2650
	2690	2700	2710	2720	2730	2740	2750
Hum.	ATGAACACCAAACATCTAAACAATCATATGCTAA-CATGC--CAC--TCCTGGAAACT-CCACTCTGAA						
	: :::: : :::::::::: ::::::::::: . . ::::: : ::::: ::::: ::::: ::::: :::::						
Mur.	ACAAAC-CTAAGCATCCGAGCAAGCTGGGGCTATT CCTGCAAAACTCCATCCTGAACGCTGTCACTCTAGA						
	2660	2670	2680	2690	2700	2710	2720

Fig. 27R

	2760	2770	2780	2790	2800	2810
Hum.	---GCTGCCGCTTTGGACACCAACTCCCTTCT-CCCAGG-GTCATGCAGGGATCTGCTCCCTCCTGC					
	2730	2740	2750	2760	2770	2780
Mur.	AGCAGCTGCTGCTTTGAACACACGCCCACCCCTCCTTCCCAAGAGTCTCTATGGAGTTGGC-CCCTTGTGT					
	2820	2830	2840	2850	2860	2870
Hum.	TTCCCTTACCAGTCGTGCACCGCTGACTCCAGGAAGTCTTTCCTGAAGTCTGACCACCTTTCTCTTCTTGC					
	2800	2810	2820	2830	2840	2850
Mur.	TTCCCTTACCAGTCGGGCCATACTGTTT---GGGAAGTCATCTCTGAAGTCTAACCACCTTCCCTTCTTGG					
	2890	2900	2910	2920	2930	2940
Hum.	TTCAGTTGGGCAGACTCTGATCCCT---TCTGCCCTGGCAGAATGGCAGGGGTAATCTGAGCCTTCTTTC					
	2860	2870	2880	2890	2900	2910
Mur.	TTCAGTTGGACAGATTGTTATTATTGTCCTCTGCCCTGGCTAGAAATGGGGCATAATCTGAGCCTTGTTTC					
	2960	2970	2980	2990	3000	3010
Hum.	ACTCCTTTACCC---TAGCTGACCCCTTCACCTCTCCC--CCTCCCTTTTCCCTTGTGTTTGGGATTCAGA					
	2930	2940	2950	2960	2970	2980
Mur.	---CCTTGTCAGTGTGGCTGACCC-TTGACCTCTTCCCTTCCCTCC---TCCCTTTGTTTGGGATTCAGA					

Fig. 27S

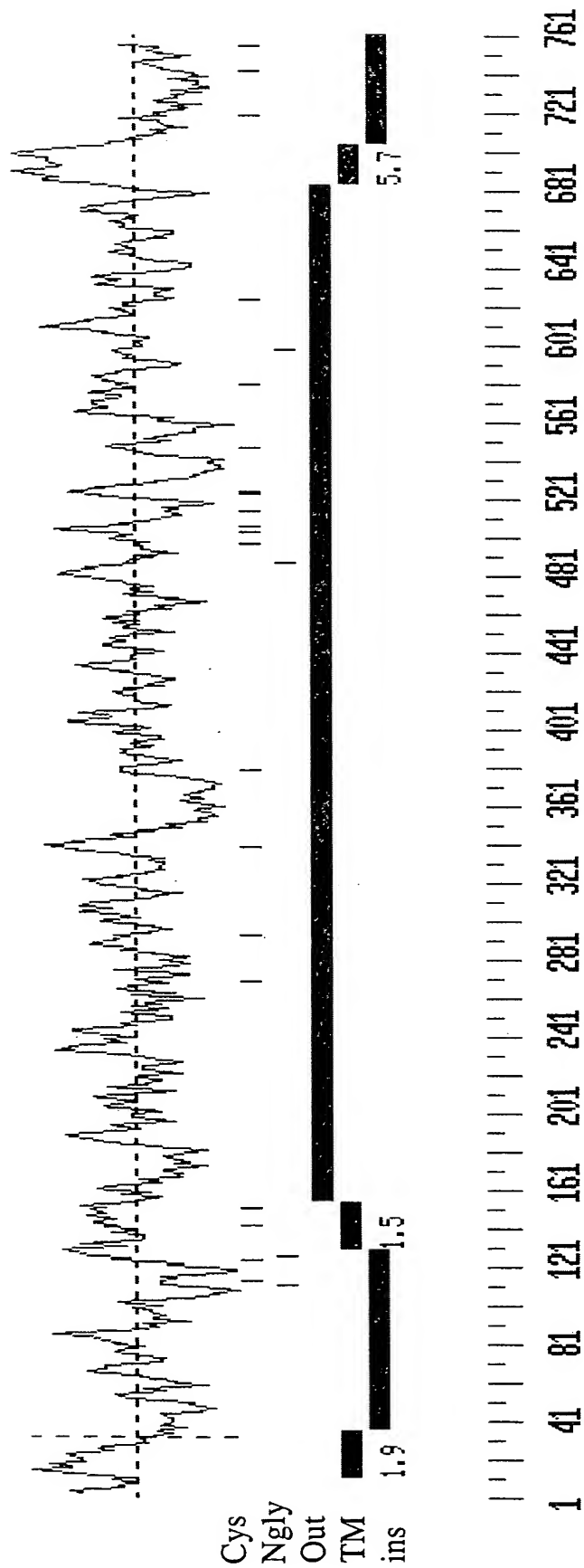


Fig. 27U

GTCGACCCACGCGTCCGACGCTTTGGACACTTTCCTCTGCTTGAGGACACCTTGACTAACCTCCAAGGGCAACTAAAGGA	79
<div style="text-align: center;">M C T K T I</div>	
TCAAGAAAGGCCAGCACAGCAGAGATCAGCTGGATCTAGCTCCTGCAGGAG ATG TGT ACA AAG ACA ATC	150
P V L W G C F L L L W N L Y V S S S Q T I	26
CCA GTC CTC TGG GGA TGT TTC CTC CTC TGG AAT CTC TAT GTC TCA TCC TCT CAG ACC ATT	210
Y P G I K A R I T Q R A L D Y G V Q A G	46
TAC CCT GGA ATC AAG GCA AGG ATT ACT CAG AGG GCA CTT GAC TAT GGT GTT CAA GCT GGA	270
M K M I E Q M L L K E K K L P D L S G S E	66
ATG AAG ATG ATT GAG CAA ATG CTA AAA GAA AAG AAA CTC CCA GAT TTA AGC GGT TCT GAG	330
S L E F L K V D Y V N Y N F S N I K I S	86
TCT CTT GAA TTT CTA AAA GTT GAT TAT GTA AAC TAC AAT TTT TCA AAT ATA AAA ATC AGT	390
A F S F P N T S L A F V P G V G I K A L	106
GCC TTT TCA TTT CCA AAT ACC TCA TTG GCT TTT GTG CCT GGA GTG GGA ATC AAA GCG CTA	450
T N H G T A N I S T D W G F E S P L F V	126
ACC AAC CAT GGC ACT GCC AAC ATC AGC ACA GAC TGG GGG TTC GAG TCT CCA CTT TTT GTT	510
L Y N S F A E P M E K P I L K N L N E M	146
CTG TAT AAC TCC TTT GCT GAG CCC ATG GAG AAA CCC ATT TTA AAG AAC TTA AAT GAA ATG	570

Fig. 28A

L	C	P	I	I	A	S	E	V	K	A	L	N	A	N	L	S	T	L	E	166
CTC	TGT	CCC	ATT	ATT	GCA	AGT	GAA	GTC	AAA	GCG	CTA	AAT	GCC	AAC	CTC	AGC	ACA	CTG	GAG	630
V	L	T	K	I	D	N	Y	T	L	L	D	Y	S	L	I	S	S	P	E	186
GTT	TTA	ACC	AAG	ATT	GAC	AAC	TAC	ACT	CTG	CTG	GAT	TAC	TCC	CTA	ATC	AGT	TCT	CCA	GAA	690
I	T	E	N	Y	L	D	L	N	L	K	G	V	F	Y	P	L	E	N	L	206
ATT	ACT	GAG	AAC	TAC	CTT	GAC	CTG	AAC	TTG	AAG	GGT	GTA	TTT	TAC	CCA	CTG	GAA	AAC	CTC	750
T	D	P	P	F	S	P	V	P	F	V	L	P	E	R	S	N	S	M	L	226
ACC	GAC	CCC	CCC	TTC	TCA	CCA	GTT	CCT	TTT	GTG	CTC	CCA	GAA	CGC	AGC	AAC	TCC	ATG	CTC	810
Y	I	G	I	A	E	Y	F	F	K	S	A	S	F	A	H	F	T	A	G	246
TAC	ATT	GGA	ATC	GCC	GAG	TAT	TTC	TTT	AAA	TCT	GCG	TCC	TTT	GCT	CAT	TTC	ACA	GCT	GGG	870
V	F	N	L	T	L	S	T	E	E	I	S	N	H	F	V	Q	N	S	Q	266
GTT	TTC	AAT	CTC	ACT	CTC	TCC	ACC	GAA	GAG	ATT	TCC	AAC	CAT	TTT	GTT	CAA	AAC	TCT	CAA	930
G	L	G	N	V	L	S	R	I	A	E	I	Y	I	L	S	Q	P	F	M	286
GGC	CTT	GGC	AAC	GTG	CTC	TCC	CGG	ATT	GCA	GAG	ATC	TAC	ATC	TTG	TCC	CAG	CCC	TTC	ATG	990
V	R	I	M	A	T	E	P	P	I	I	N	L	Q	P	G	N	F	T	L	306
GTG	AGG	ATC	ATG	GCC	ACA	GAG	CCT	CCC	ATA	ATC	AAT	CTA	CAA	CCA	GGC	AAT	TTC	ACC	CTG	1050
D	I	P	A	S	I	M	M	L	T	Q	P	K	N	S	T	V	E	T	I	326
GAC	ATC	CCT	GCC	TCC	ATC	ATG	ATG	CTC	ACC	CAA	CCC	AAG	AAC	TCC	ACA	GTT	GAA	ACC	ATC	1110

Fig. 28B

V	S	M	D	F	V	A	S	T	S	V	G	L	V	I	L	G	Q	R	L	346
GTT	TCC	ATG	GAC	TTC	GTT	GCT	AGT	ACC	AGT	GTT	GGC	CTG	GTT	ATT	TTG	GGA	CAA	AGA	CTG	1170
V	C	S	L	S	L	N	R	F	R	L	A	L	P	E	S	N	R	S	N	366
GTC	TGC	TCC	TTG	TCT	CTG	AAC	AGA	TTC	CGC	CTT	GCT	TTG	CCA	GAG	TCC	AAT	CGC	AGC	AAC	1230
I	E	V	L	R	F	E	N	I	L	S	S	I	L	H	F	G	V	L	P	386
ATT	GAG	GTC	TTG	AGG	TTT	GAA	AAT	ATT	CTA	TCG	TCC	ATT	CTT	CAC	TTT	GGA	GTC	CTC	CCA	1290
L	A	N	A	K	L	Q	Q	G	F	P	L	P	N	P	H	K	F	L	F	406
CTG	GCC	AAT	GCA	AAA	TTG	CAG	CAA	GGA	TTT	CCT	CTG	CCC	AAT	CCA	CAC	AAA	TTT	TTA	TTC	1350
V	N	S	D	I	E	V	L	E	G	F	L	L	I	S	T	D	L	K	Y	426
GTC	AAT	TCA	GAT	ATT	GAA	GTT	CTT	GAG	GGT	TTC	CTT	TTG	ATT	TCC	ACC	GAC	CTG	AAG	TAT	1410
E	T	S	S	K	Q	Q	P	S	F	H	V	W	E	G	L	N	L	I	S	446
GAA	ACA	TCC	TCA	AAG	CAG	CAG	CCA	AGT	TTC	CAC	GTA	TGG	GAA	GGT	CTG	AAC	CTG	ATA	AGC	1470
R	Q	W	R	G	K	S	A	P	*											456
AGA	CAG	TGG	AGG	GGG	AAG	TCA	GCC	CCT	TGA											1500
TTGCCGGTTTGCAATTCA	CCCCAGGAAAGTAAATGGTCCCTTAATCCTACAACTACTGTAAACCCAGAGGAAAGACAGT	1579																		
ACACACTGGAATTGTAAAGCCCTTGTGAATTGCTTAGGCAGAAAGTTTCTTTAAGCCCTTCAGGAACCCAGATAA	1658																			
GGCAGACTCTGTAAAGGGATAAATAGAGGTGTCTGAATGTGAGTGTATGCATGCTGCGTGTGTCTGTGTTATGTTG	1737																			
TTTGTTTGTTGGGCAAGAAAGATTCTAGGACAAAGAGCTAGGCATGTACTTCTGACCCAGGTGGGTAAGCAACTCTAAG	1816																			

Fig. 28C

TCTGTATTGTATTGGTCATTCTCAGTGGAAATCCCTTAGGCCCTCTAGTGGTTTTTCCCCCTACCTGCATATAATTGGTTTTC 1895
ATGTTTTATATTCACTGTACTATCTTCTCTGTGTTTAAATTAAATTGTTTTTCTATCAAAAAAAAAAAAAAAAAAAGGGC 1974
GGCCGC 1980

Fig. 28D

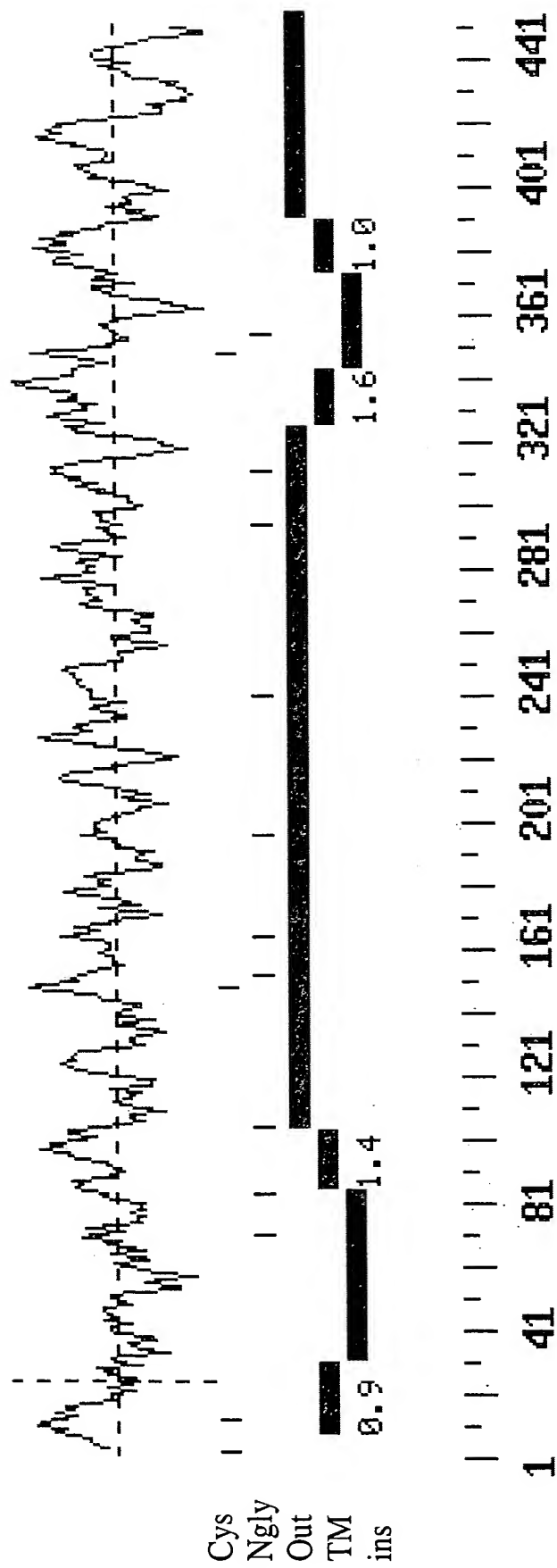


Fig. 28E

```

10      20      30      40      50      60
286 MCTKT-IPVLWGCFL-LWNLVSSSQTIYPGIKARITQRALDYGVAQGMKMIQMLKEKKLPDLGSES
:      :      :      :      :      :      :      :      :      :      :
BPI MARGPCNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS--DSF
10      20      30      40      50      60

70      80      90      100     110     120     130
286 EFLKVDYVNYNFSNIKISAFSPNTSLAFVPGVGIKALTNHGTANISTDWGFESPLFVLVNSFAEPME--
.      .      .      .      .      .      .      .      .      .      .
BPI KIKHLGKGHSFYFMDIREFQLPSSQISMVNPVGLKFISNANIKISGKWKAKRFLKMSGNFDLSIEGM
70      80      90      100     110     120     130

286 -----KPI-----140      150
:      :      :      :      :      :      :      :      :      :      :
BPI SISADLKLGSNPTSGKPTITCSSSCSHINSVHVHISKSKVGWLIQLFHKKIESALRNKMNSQVCEKVTNS
140     150     160     170     180     190     200

160     170     180     190     200     210     220
286 VKA-LNANLSTLEVLTKIDNYTLDDYSLISSPEITENYLDNLKGVFYPLENLTDPFSPVFLPERSN
:      :      :      :      :      :      :      :      :      :      :
BPI VSSKLQPYFQTLFVMTKIDSVAGINYLVAAPPATTAETLDVQMKGEFYSENHHNPPFPFAPVMEFFAAHD
210     220     230     240     250     260     270

```

Fig. 28F

[illegible]

```

10      20      30      40      50      60
286 MCTKTIPVLWGCFLWNLYVSSSQTI--YPGIKARITQRALDYGVQAGMKMIEQMLKEKKLPDLGSGSESL
: . . . . . : : : : : : : : : : : : : : : : : : : : : : : :
RENP MGALARAL--PSILLALLTSTPEALGANPGLVARITDKGLQYAAQEGLLALQSELLRITLPDFTG--DL
10      20      30      40      50      60

70      80      90      100     110     120     130
286 EFLKVDYVNYNFSNIKISAFSPNTSLAFVPGVGIKALTNHGTANISTDWGFESPLFVLYNSFAEPME--
. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :.
RENP RIPHVGRGRYEFHSLNIHEFQLPSSQISMVPNVGLKFSISNANIKISGKWKAQKRFLKMSGNFDLSIEGM
70      80      90      100     110     120     130

140      150
286 -----KPI-----LKN-LNEMLCPIIASE
: :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :.
RENP SISADLKLGSNPTSGKPTITCSCSCSSHINSVHVHISKSKVGWLIQLFHKKIESALRNKMNSQVCEKVTNS
140      150      160      170      180      190      200

160      170      180      190      200      210      220
286 VKA-LNANLSTLEVLTKIDNYTLTDYSLISSPEITENYLDLNLKGVFYPLENLTDPFSPVFFVLPERSN
: . :. . :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :.
RENP VSSKLQPYFQTLPMTKIDSVAGINYLVAAPPATTAETLDVQMKGEFYSENHHNPPPFAPPVMEFPAAHD
210      220      230      240      250      260      270

```

Fig. 28H

Fig. 28I

GTCGACCCACGCGTC	CGGGAATTGCAGCAGG	AAATATGTGAAGAGT	TTTTAAACCCACAA	ATTCTTCTTACTTTAGA	79
<div style="text-align: center;">M L E T L S R Q</div>					8
ATTAGTTGTTACAT	TGGCAGGAAAAATAA	TGCAGATGTTGGACC	ATG TTG GAA ACC	TTG TCA AGA CAG	149
W I V S H R M E M	W L L I L V A Y M	F Q			28
TGG ATT GTC TCA	CAC AGA ATG GAA	ATG TGG CTT CTG	ATT CTG GTG GCG	TAT ATG TTC CAG	209
R N V N S V H M P	T K A V D P E A	F M N			48
AGA AAT GTG AAT	TCA GTA CAT ATG	CCA ACT AAA GCT	GTG GAC CCA GAA	GCA TTC ATG AAT	269
I S E I I Q H Q G	Y P C E E Y E	V A T E			68
ATT AGT GAA ATC	CAA CAT CAA GGC	TAT CCC TGT GAG	GAA TAT GAA GTC	GCA ACT GAA	329
D G Y I L S V N R	I P R G L V Q	P K K T			88
GAT GGG TAT ATC	CTT TCT GTT AAC	AGG ATT CCT CGA	GGC CTA GTG CAA	CCT AAG AAG ACA	389
G S R P V V L L Q	H G L V G A S	N W I			108
GGT TCC AGG CCT	GTG GTG TTA CTG	CAG CAT GGC CTA	GTT GGA GGT GCT	AGC AAC TGG ATT	449
S N L P N N S L G	F I L A D A G	F D V W			128
TCC AAC CTG CCC	AAC AAT AGC CTG	GGC TTC ATT CTG	GCA GAT GCT GGT	TTT GAC GTG TGG	509
M G N S R G N A W	S R K H K T L S	I D Q			148
ATG GGG AAC AGC	AGG GGA AAC GCC	TGG TCT CGA AAA	CAC AAG ACA CTC	TCC ATA GAC CAA	569

Fig. 29A

D	E	F	W	A	F	S	Y	D	E	M	A	R	F	D	L	P	A	V	I	168
GAT	GAG	TTC	TGG	GCT	TTC	AGT	TAT	GAT	GAG	ATG	GCT	AGG	TTT	GAC	CTT	CCT	GCA	GTG	ATA	629
N	F	I	L	Q	K	T	G	Q	E	K	I	Y	Y	V	G	Y	S	Q	G	188
AAC	TTT	ATT	TTG	CAG	AAA	ACG	GGC	CAG	GAA	AAG	ATC	TAT	TAT	GTC	GGC	TAT	TCA	CAG	GGC	689
T	T	M	G	F	I	A	F	S	T	M	P	E	L	A	Q	K	I	K	M	208
ACC	ACC	ATG	GGC	TTT	ATT	GCA	TTT	TCC	ACC	ATG	CCA	GAG	CTG	GCT	CAG	AAA	ATC	AAA	ATG	749
Y	F	A	L	A	P	I	A	T	V	K	H	A	K	S	P	G	T	K	F	228
TAT	TTT	GCT	TTA	GCA	CCC	ATA	GCC	ACT	GTT	AAG	CAT	GCA	AAA	AGC	CCC	GGG	ACC	AAA	TTT	809
L	L	L	P	D	M	M	I	K	G	L	F	G	K	K	E	F	L	Y	Q	248
TTG	TTG	CTG	CCA	GAT	ATG	ATG	ATC	AAG	GGA	TTG	TTT	GGC	AAA	AAA	GAA	TTT	CTG	TAT	CAG	869
T	R	F	L	R	Q	L	V	I	Y	L	C	G	Q	V	I	L	D	Q	I	268
ACC	AGA	TTT	CTC	AGA	CAA	CTT	GTT	ATT	TAC	CTT	TGT	GGC	CAG	GTG	ATT	CTT	GAT	CAG	ATT	929
C	S	N	I	M	L	L	L	G	G	F	N	T	N	N	M	N	M	S	R	288
TGT	AGT	AAT	ATC	ATG	TTA	CTT	CTG	GGT	GGA	TTC	AAC	ACC	AAC	AAT	ATG	AAC	ATG	AGC	CGA	989
A	S	V	Y	A	A	H	T	L	A	G	T	S	V	Q	N	I	L	H	W	308
GCA	AGT	GTA	TAT	GCT	GCC	CAC	ACT	CTT	GCT	GGA	ACA	TCT	GTG	CAA	AAT	ATT	CTA	CAC	TGG	1049
S	Q	A	V	N	S	G	E	L	R	A	F	D	W	G	S	E	T	K	N	328
AGC	CAG	GCA	GTG	AAT	TCT	GGT	GAA	CTC	CGG	GCA	TTT	GAC	TGG	GGG	AGT	GAG	ACC	AAA	AAT	1109

Fig. 29B

[illegible]

Fig. 29C

```

10      20      30      40      50      60      70
294 MLETLRQWIVSHRMEMWLLILVAYMFQNNVNSVHMPTKAVDPEAFMNISEIIHQGYPCEEYEVATEDG
:      . . . : : : . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
HLP M-----WLL---LTMASLISVLGTTGHLGFKLH-----PGSPEVTMNISQMITYWGYPNEEYEVVTTEDG
      10      20      30      40      50

      80      90      100      110      120      130      140
294 YILSVNRIPRGLVQPKKTGSRPVVLLQHGLVGGASNWISNLPNNSLGFILADAGFDVWMGNSRGNWSRK
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
HLP YILEVNRIPYGKKNSGNTGQRPVVFLQHGLLASATNWISNLPNNSLAFILADAGYDVWLGNRGNWTWARR
      60      70      80      90      100      110      120

      150      160      170      180      190      200      210
294 HKTLSIDQDEFWAFSYDEMARFDLPAVINFILQKTQGEKIYVVGYSQGTMGFIAFSTMPELAQKIKMYF
. : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
HLP NLYYSPDSVEFWAFSFDDEMAKYDLPATIDFIVKKTGQKQLHYVGHVSQGTIGFIAFSTNPSLAKRIKTFY
      130      140      150      160      170      180      190

      220      230      240      250      260      270
294 ALAPIATVKHAKSPGTKFLLLPDMMIKGLFGKKEFLYQTRFLRQ-LVIYLCGQVILDQICSNIMLLLGGF
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
HLP ALAPVATVKYTKSLINKLRFVPQSLFKFIFGDKIF-YPHNFFDQFLATEVCSREMLNLLCSNALFIICGF
      200      210      220      230      240      250      260

```

Fig. 29D

```

280      290      300      310      320      330      340
294 NTNNMMSRASVYAAHTLAGTSVQNILHWSQAVNSGELRAFDWGSETKNLEKCNQPTPVRYRVRDMTVPT
... : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
HLP DSKNFNTSRLLDVYLSHNPAGTSVQNMFWHTQAVKSGKFQAYDWGSPVQNRMHYDQSQPPYYNVVTAMNVPI
270      280      290      300      310      320      330

350      360      370      380      390      400      410
294 AMWTGGQDWLSNPEDVKMLLSEVTNLIYHKNIPEWAHVDFIWGLDAPHRMYNEIIHLMQQEETNLSQGR
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
HLP AVWNGGKDLLADPPQDVGLLPKLPNLIYHKEIPFYNHLDFIWAMDAPQEVYNDIVSMISEDKK-----
340      350      360      370      380      390

420
294 EAVL

HLP ----

```

Fig. 29E

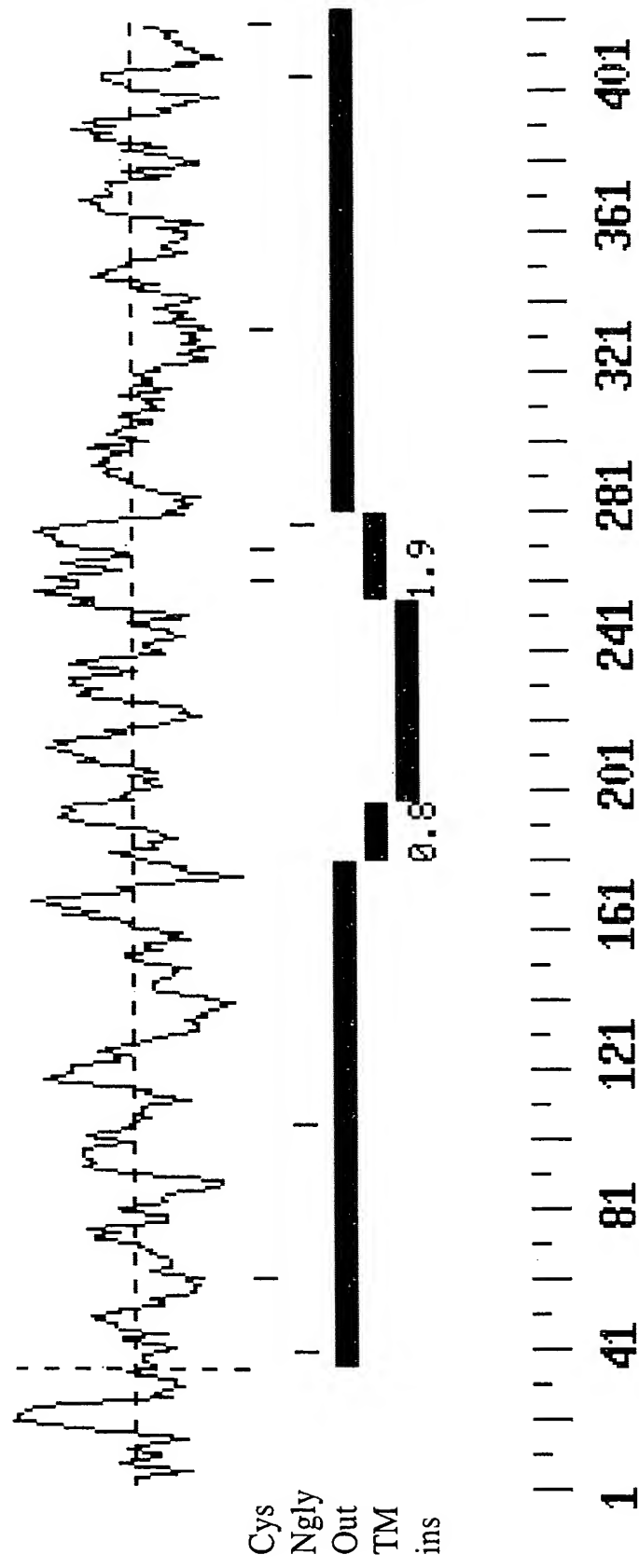


Fig. 29F

```

10      20      30      40      50      60
294 MLETLRQWIVSHRMEMWLLILVAYMFQNNVNSVHMPK--AVDPEAFMNISEIIQHQQYPCEEYEVATE
:      :...: . . . . :      :      :      :      :      :      :
LAL M-----KMRFLGLVVCLVWLPLHSEGGKLTAVDPETNMNVSEIISYWGFPSSEYYLVETE
      10      20      30      40      50

70      80      90      100     110     120     130
294 DGYILSVNRIPRGLVQPKKTGSRPVVLLQHGLVGGASNWISNLPNNSLGFILADAGFDVWMGNSRGNAWS
:      :      : . . . . . :      :      :      :      :      :      :
LAL DGYILCLNRI PHGRKNHSDKGPVVF LQHGLLADSSNWVTNLANSSLGFILADAGFDVWMGNSRGNTWS
      60      70      80      90      100     110     120

140     150     160     170     180     190     200
294 RKHKTLSDQDEFWAFSYDEMAREFDLPVAVINFILQKTGQEKIYVVGYSQGTMTMGFI AFSTMP ELAQIKM
:      :      :      :      :      :      :      :      :      :      :
LAL RKHKTLVSQDEFWAFSYDEMAKYDLPASINFILNKTGQEQVYVVGHSQGTTFIAFSQIPELAKRIKM
      130     140     150     160     170     180     190

210     220     230     240     250     260     270
294 YFALAPIATVKHAKSPGTKFLLLPDMMIKGLFGKKEFLYQTRFLRQLVIYLCGQVILDQICSNIMLLGG
:      :      : . . . : : : : : : : : : : : : : : : : : : :
LAL FFALGPVASVAFCTSPMAKLGRLPDHLIKDLFGDKFELPQSAFLKWLGTHVTHVILKELCGNLCFLLCG
      200     210     220     230     240     250     260

```

Fig. 29G

```

280      290      300      310      320      330      340
294 FNTNNMMSRASVYAAHTLAGTSVQNILHWSQAVNSGELRAFDWGSETKNLEKCNQPTPVRYRVRDMTVP
   :: :::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
LAL FNERNLNMSRVDVYTTHTSPAGTSVQNMLHWSQAVKFKQAFDWGSSAKNYFHYNQSYPPPTYNVKDMLVP
270      280      290      300      310      320      330

350      360      370      380      390      400      410
294 TAMWTGGQDWLSNPEDVKMLLSEVTNLIYHKNIPEWAHVDFIWGLDAPHRMYNEIIHLMQQEETNLSQGR
   :::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
LAL TAVWSSGGHDWLADVVDVNILLTQITNLFHESIPWEHLDFIWGLDAPWRLYNKIIINLMRKYQ-----
340      350      360      370      380      390

420
294 CEAVL

LAL -----

```

Fig. 29H

GTCGACCCACGCGTCCACGGCAGGGCTCCCGGGCGCAGCATTTGCCCCCCTGCACCACCTCACCAAG	ATG	GCT	75
T L G H T F P F Y A G P K P T F P M D T			22
ACT TTG GGA CAC ACA TTC CCC TTC TAT GCT GGC CCC AAG CCA ACC TTC CCG ATG GAC ACC			135
T L A S I I M I F L T A L A T F I V I L			42
ACT TTG GCC AGC ATC ATC ATG ATC TTT CTG ACT GCA CTG GCC ACG TTC ATC GTC ATC CTG			195
P G I R G K T R L F W L L R V V T S L F			62
CCT GGC ATT CGG GGA AAG ACG AGG CTG TTC TGG CTG CTT CGG GTG GTG ACC AGC TTA TTC			255
I G A A I L A V N F S S E W S V G Q V S			82
ATC GGG GCT GCA ATC CTG GCT GTG AAT TTC AGT TCT GAG TGG TCT GTG GGC CAG GTC AGC			315
T N T S Y K A F S S E W I S A D I G L Q			102
ACC AAC ACA TCA TAC AAG GCC TTC AGT TCT GAG TGG ATC AGC GCT GAT ATT GGG CTG CAG			375
V G L G G V N I T L T G T P V Q Q L N E			122
GTC GGG CTG GGT GGA GTC AAC ATC ACA CTC ACA GGG ACC CCC GTG CAG CAG CTG AAT GAG			435
T I N Y N E E F T W R L G E N Y A E E C			142
ACC ATC AAT TAC AAC GAG GAG TTC ACC TGG CGC CTG GGT GAG AAC TAT GCT GAG GAG TGT			495
A K A L E K G L P D P V L Y L A E K F T			162
GCA AAG GCT CTG GAG AAG GGG CTG CCA GAC CCT GTG TTG TAC CTA GCT GAG AAG TTC ACT			555

Fig. 30A

P	R	S	P	C	G	L	Y	R	Q	Y	R	L	A	G	H	Y	T	S	A	182	
CCA	AGA	AGC	CCA	TGT	GGC	CTA	TAC	TAC	CGC	CAG	TAC	CGC	CTG	GCG	GGA	CAC	TAC	ACC	TCA	GCC	615
M	L	W	V	A	F	L	C	W	L	L	A	N	V	M	L	S	M	P	V	202	
ATG	CTA	TGG	GTG	GCA	TTC	CTC	TGC	TGG	CTG	CTG	GCC	AAT	GTG	ATG	CTC	TCC	ATG	CCT	GTG	675	
L	V	Y	G	G	Y	M	L	L	A	T	G	I	F	Q	L	L	A	L	L	222	
CTG	GTA	TAT	GGT	GGC	TAC	ATG	CTA	TTG	GCC	ACG	GGC	ATC	TTC	CAG	CTG	TTG	GCT	CTG	CTC	735	
F	F	S	M	A	T	S	L	T	S	P	C	P	L	H	L	G	A	S	V	242	
TTC	TTC	TCC	ATG	GCC	ACA	TCA	CTC	ACC	TCA	CCC	TGT	CCC	CTG	CAC	CTG	GGC	GCT	TCT	GTG	795	
L	H	T	H	H	G	P	A	F	W	I	T	L	T	T	G	L	L	C	V	262	
CTG	CAT	ACT	CAC	CAT	GGG	CCT	GCC	TTC	TGG	ATC	ACA	TTG	ACC	ACA	GGA	CTG	CTG	TGT	GTG	855	
L	L	G	L	A	M	A	V	A	H	R	M	Q	P	H	R	L	K	A	F	282	
CTG	CTG	GGC	CTG	GCT	ATG	GCG	GTG	GCC	CAC	AGG	ATG	CAG	CCT	CAC	AGG	CTG	AAG	GCT	TTC	915	
F	N	Q	S	V	D	E	D	P	M	L	E	W	S	P	E	E	G	G	L	302	
TTC	AAC	CAG	AGT	GTG	GAT	GAA	GAC	CCC	ATG	CTG	GAG	TGG	AGT	CCT	GAG	GAA	GGT	GGA	CTC	975	
L	S	P	R	Y	R	S	M	A	D	S	P	K	S	Q	D	I	P	L	S	322	
CTG	AGC	CCC	CGC	TAC	CGG	TCC	ATG	GCT	GAC	AGT	CCC	AAG	TCC	CAG	GAC	ATT	CCC	CTG	TCA	1035	
E	A	S	S	T	K	A	Y	C	K	E	A	H	P	K	D	P	D	C	A	342	
GAG	GCT	TCC	TCC	ACC	AAG	GCA	TAC	TGT	AAG	GAG	GCA	CAC	CCC	AAA	GAT	CCT	GAT	TGT	GCT	1095	

Fig. 30B

L	*	344
TTA	TAA	1101
CATTCCTCCCGTGGAGGCCACCTGGACTTCCAGTCTGGCTCCAAACCTCATTTGGCGCCCCATAAAACCAGCAGAACTG		1180
CCCTCAGGGTGGCTGTTACCAAGACACCCAGCACCAATCTACAGACGGAGTAGAAAAAGGAGGCTCTATATACTGATGTT		1259
AAAAACAAAACAAAACAAAAGCCCTAAGGACCTGAAGAGATGCTGGCCCTGTCCATAAAGCCCTGTTGCCATGATAAG		1338
GCCAAGCAGGGCTAGCTTATCTGCACAGCAACCCAGCCTTCCGTGCTGCCCTTGCCCTCTTCAAGATGCTATTCACTGA		1417
AACCTAACTTCAACCCCATAAACACAGCAGGTGGGGTTACATAATGATTCTCCATATGGTTTCCCTCATCCCTCGGCA		1496
CCCTTGTTTTCCTTTTCCCTGGGTTCCCTTTTGTTCTTCTTACTTCTCCAGCTTGTGTGGCCTTTTGGTACAATGAA		1575
AGACAGCACTGGAAGGAGGGGAAACCAACCTTCTCATCCTAGGCTAAACATTAAACCAACTATGCCACATTCTCTTTGA		1654
GCTTCAGTTCCTCCAAATTTGCTACATAAGATTGCAAGACTTGCCCAAGAAATCTTGGGATTTATCTTTCATGCTTGCTGA		1733
CACCTACCTTGGCCCTCAAACACACCTCACAGAAGCCAGGTGGGAAGTAGGGAATCAACTCCAACGCTATTCCT		1812
TCCCACCCCACTCAGCTGGGCTAGCTGAGTGGCATCCAGGACGGGGAGTGGTGACCTGCCCTCATCACTGCCACCTAA		1891
CGTCCCCCTGGGTGTTCAAGATGCTAGCTCTGGTAGGGTCCCTCCGGCCCTCACTAGAGGGCCCCCTATTACTC		1970
TGGAGTCGACGCAGAGAAATCAGGTTTTCACAGCACTGCGGAGAGTGTAAGCTGTCTCCAGCCAGCGAAGCTCATGA		2049
GGACGTGCGACCCCGCGCGGAGAAAGCCATGAAAATTATGGGAAAAAACAGTTTTTAAAAAATAAAAAAAGGGCG		2128
GCCGC		2133

Fig. 30C

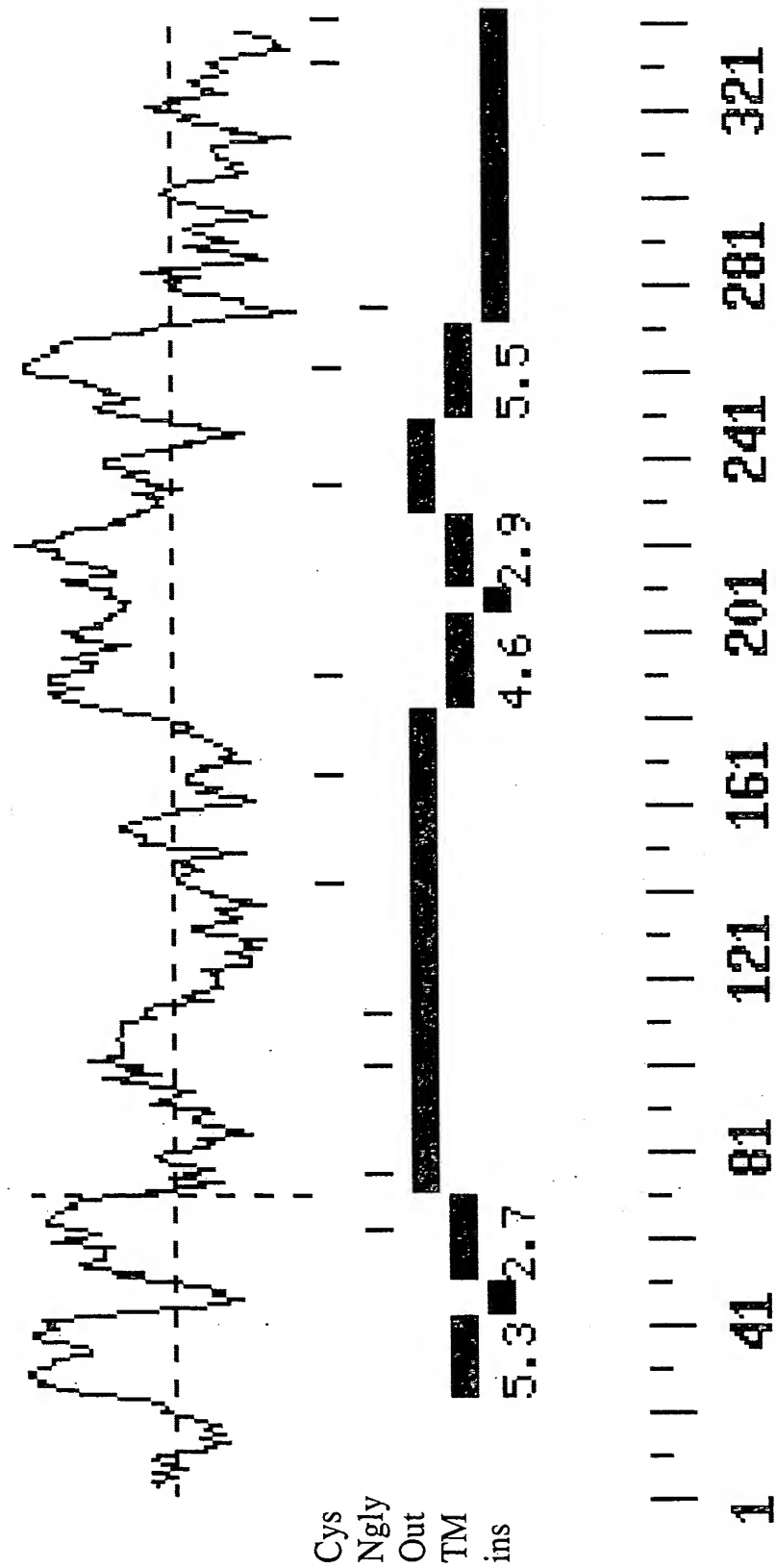


Fig. 30D

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10      20      30      40      50      60      70
296 · MATLGHTFPFYAGPKPTFPMDTTLASIMIFLTALATFIVILPGIRGKTRLFWLLRVVTSLSFIGAAILAV
:  ::  :...  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::
CRP M-RIAH-----ASSRGN-----SIFSFLIPLIAIYLILPGVR-RKRVVTTVTYVLMMLAVGGALIAS
10      20      30      40      50

80      90      100     110     120     130
296 NFSSEWSVGQVSTNTSYKAFSSEWISADIGLQVGLGVNITL-----TGTPVQQLNETIN--YNEEFTW
.  .  .  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
CRP LIYPCWASGSQMIYTQFRGHSNERILAKIGVEIGLQKVNVTLKFERLLSSNDVLPGSDMTELYYNEGFDI
60      70      80      90      100     110     120

140     150     160     170     180     190     200
296 RLGENYAECAKALEKGLPDPVLYLAEKFT-PRSPCGLYRQYRLAGHYTSAMLWVAFLCWLLANV-MLSM
.  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .
CRP SGISSMAEALHHGLENGLPYPMLSVLEYFSLNQDSFDWGRHYRVAGHYTHAAIWFAFACWCLSVVLMLFL
130     140     150     160     170     180     190

210     220     230     240     250     260
296 PVLVYGGYMLLATGIFQLLALLFFSMATSLTSPCPLHL---GASVLHTHHGPAF---WITLTTGLLCVL
:  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .
CRP PHNAYKS--ILATGISCLIACLVYL---LLSPCELRIAFGTGENFERVDLTATFSFCFYLLIFAIGILCVL
200     210     220     230     240     250     260

```

Fig. 30E


```

270      280      290      300      310      320
296 LGLAMAVAHRMQPHRLKAFFNQSVDEDPMLEW-----SPEEGLLSPRY--RSMADSPKSQDIPLSEAS
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CRP CGLGLGICEHWRIYTLSTFLDASLDEHVGPWKKKLPTGGPALQGVQIGAYGTNTTNSSRDKNDISSDKTA
270      280      290      300      310      320      330

330
296 STKAY-----CK-----EAHPKDPD-----CA----L
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CRP GSSGFQSRSTCQSSASSASLRSQSSIETVHDEAELEERTHVHFLQEPCCSSSST
340      350      360      370      380

```

Fig. 30F